

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Kohei MIYAZONO; Takeshe IMAMURA; Peter DEN DIJKE
- (ii) TITLE OF INVENTION: ISOLATED ALK-1 PROTEIN, NUCLEIC ACIDS ENCODING IT, AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 29
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Fulbright & Jaworski L.L.P.
  - (B) STREET: 666 Fifth Avenue
  - (C) CITY: New York City
  - (D) STATE: New York
  - (E) COUNTRY: USA
  - (F) ZIP: 10103
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
  - (B) COMPUTER: IBM PS/2
  - (C) OPERATING SYSTEM: PC-DOS
  - (D) SOFTWARE: Wordperfect
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: 09/039,177
  - (B) FILING DATE: March 13, 1998
  - (C) CLASSIFICATION: 435
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: PCT/GB93/02367
  - (B) FILING DATE: November 17, 1993
- See 32* (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: GB 9224057.1
  - (B) FILING DATE: November 17, 1992
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: GB 9304677.9
  - (B) FILING DATE: March 8, 1993
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: GB 9304680.3
  - (B) FILING DATE: March 8, 1993
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 9311047.6
  - (B) FILING DATE: May 28, 1993
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 9313763.6
  - (B) FILING DATE: July 2, 1993

## (vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 9136099.2  
 (B) FILING DATE: August 3, 1993

## (vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 321344.5  
 (B) FILING DATE: October 15, 1993

## (viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Mary Anne Schofield  
 (B) REGISTRATION NUMBER: 36,669  
 (C) REFERENCE/DOCKET NUMBER: LUD 5539.1 CIP - JEL/MAS

## (ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (212) 318-3000  
 (B) TELEFAX: (212) 752-5958

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1984 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (v) FRAGMENT TYPE: internal

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 283..1791

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

AGGAAACGGT TTATTAGGAG GGAGTGGTGG AGCTGGGCCA GGCAGGAAGA CGCTGGAATA 60  
 AGAAACATTT TTGCTCCAGC CCCCATCCCA GTCCCGGGAG GCTGCCGCGC CAGCTGCGCC 120  
 GAGCGAGCCC CTCCCCGGCT CCAGCCCGGT CCGGGGCCGC GCCGGACCCC AGCCCGCCGT 180  
 CCAGCGCTGG CGGTGCAACT GCGGCCGCGC GGTGGAGGGG AGGTGGCCCC GTCCGCCGA 240  
 AGGCTAGCGC CCCGCCACCC GCAGAGCGGG CCCAGAGGGA CC ATG ACC TTG GGC 294  
 Met Thr Leu Gly

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| TCC | CCC | AGG | AAA | GGC | CTT | CTG | ATG | CTG | CTG | ATG | GCC | TTG | GTG | ACC | CAG | 342 |
| Ser | Pro | Arg | Lys | Gly | Leu | Leu | Met | Leu | Leu | Met | Ala | Leu | Val | Thr | Gln |     |
| 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |     |     | 20  |     |
| GGA | GAC | CCT | GTG | AAG | CCG | TCT | CGG | GGC | CCG | CTG | GTG | ACC | TGC | ACG | TGT | 390 |
| Gly | Asp | Pro | Val | Lys | Pro | Ser | Arg | Gly | Pro | Leu | Val | Thr | Cys | Thr | Cys |     |
|     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |     | 35  |     |     |
| GAG | AGC | CCA | CAT | TGC | AAG | GGG | CCT | ACC | TGC | CGG | GGG | GCC | TGG | TGC | ACA | 438 |
| Glu | Ser | Pro | His | Cys | Lys | Gly | Pro | Thr | Cys | Arg | Gly | Ala | Trp | Cys | Thr |     |
|     |     |     | 40  |     |     |     |     | 45  |     |     |     |     | 50  |     |     |     |
| GTA | GTG | CTG | GTG | CGG | GAG | GAG | GGG | AGG | CAC | CCC | CAG | GAA | CAT | CGG | GGC | 486 |
| Val | Val | Leu | Val | Arg | Glu | Glu | Gly | Arg | His | Pro | Gln | Glu | His | Arg | Gly |     |
|     |     | 55  |     |     |     |     | 60  |     |     |     |     | 65  |     |     |     |     |
| TGC | GGG | AAC | TTG | CAC | AGG | GAG | CTC | TGC | AGG | GGG | CGC | CCC | ACC | GAG | TTC | 534 |
| Cys | Gly | Asn | Leu | His | Arg | Glu | Leu | Cys | Arg | Gly | Arg | Pro | Thr | Glu | Phe |     |
|     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |     |     |     |     |
| GTC | AAC | CAC | TAC | TGC | TGC | GAC | AGC | CAC | CTC | TGC | AAC | CAC | AAC | GTG | TCC | 582 |
| Val | Asn | His | Tyr | Cys | Cys | Asp | Ser | His | Leu | Cys | Asn | His | Asn | Val | Ser |     |
| 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |     | 100 |     |     |
| CTG | GTG | CTG | GAG | GCC | ACC | CAA | CCT | CCT | TCG | GAG | CAG | CCG | GGA | ACA | GAT | 630 |
| Leu | Val | Leu | Glu | Ala | Thr | Gln | Pro | Pro | Ser | Glu | Gln | Pro | Gly | Thr | Asp |     |
|     |     |     |     | 105 |     |     |     |     | 110 |     |     |     | 115 |     |     |     |
| CGC | CAG | CTG | GCC | CTG | ATC | CTG | GGC | CCC | GTG | CTG | GCC | TTG | CTG | GCC | CTG | 678 |
| Gly | Gln | Leu | Ala | Leu | Ile | Leu | Gly | Pro | Val | Leu | Ala | Leu | Leu | Ala | Leu |     |
|     |     |     | 120 |     |     |     |     | 125 |     |     |     |     | 130 |     |     |     |
| GTG | GCC | CTG | GGT | GTC | CTG | GGC | CTG | TGG | CAT | GTC | CGA | CGG | AGG | CAG | GAG | 726 |
| Val | Ala | Leu | Gly | Val | Leu | Gly | Leu | Trp | His | Val | Arg | Arg | Arg | Gln | Glu |     |
|     |     | 135 |     |     |     |     | 140 |     |     |     |     | 145 |     |     |     |     |
| AAG | CAG | CGT | GGC | CTG | CAC | AGC | GAG | CTG | GGA | GAG | TCC | AGT | CTC | ATC | CTG | 774 |
| Lys | Gln | Arg | Gly | Leu | His | Ser | Glu | Leu | Gly | Glu | Ser | Ser | Leu | Ile | Leu |     |
|     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |     |     |     |     |
| AAA | GCA | TCT | GAG | CAG | GGC | GAC | ACG | ATG | TTG | GGG | GAC | CTC | CTG | GAC | AGT | 822 |
| Lys | Ala | Ser | Glu | Gln | Gly | Asp | Thr | Met | Leu | Gly | Asp | Leu | Leu | Asp | Ser |     |
| 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |     | 180 |     |     |
| GAC | TGC | ACC | ACA | GGG | AGT | GGC | TCA | GGG | CTC | CCC | TTC | CTG | GTG | CAG | AGG | 870 |
| Asp | Cys | Thr | Thr | Gly | Ser | Gly | Ser | Gly | Leu | Pro | Phe | Leu | Val | Gln | Arg |     |
|     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |     | 195 |     |     |
| ACA | GTG | GCA | CGG | CAG | GTT | GCC | TTG | GTG | GAG | TGT | GTG | GGA | AAA | GGC | CGC | 918 |
| Thr | Val | Ala | Arg | Gln | Val | Ala | Leu | Val | Glu | Cys | Val | Gly | Lys | Gly | Arg |     |
|     |     |     | 200 |     |     |     |     | 205 |     |     |     |     | 210 |     |     |     |
| TAT | GGC | GAA | GTG | TGG | CGG | GGC | TTG | TGG | CAC | GGT | GAG | AGT | GTG | GCC | GTC | 966 |
| Tyr | Gly | Glu | Val | Trp | Arg | Gly | Leu | Trp | His | Gly | Glu | Ser | Val | Ala | Val |     |
|     |     | 215 |     |     |     |     | 220 |     |     |     |     | 225 |     |     |     |     |

AAG ATC TTC TCC TCG AGG GAT GAA CAG TCC TGG TTC CGG GAG ACT GAG 1014  
 Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe Arg Glu Thr Glu  
 230 235 240

ATC TAT AAC ACA GTA TTG CTC AGA CAC GAC AAC ATC CTA GGC TTC ATC 1062  
 Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile Leu Gly Phe Ile  
 245 250 255 260

GCC TCA GAC ATG ACC TCC CGC AAC TCG AGC ACG CAG CTG TGG CTC ATC 1110  
 Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln Leu Trp Leu Ile  
 265 270 275

ACG CAC TAC CAC GAG CAC GGC TCC CTC TAC GAC TTT CTG CAG AGA CAG 1158  
 Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe Leu Gln Arg Gln  
 280 285 290

ACG CTG GAG CCC CAT CTG GCT CTG AGG CTA GCT GTG TCC GCG GCA TGC 1206  
 Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val Ser Ala Ala Cys  
 295 300 305

GGC CTG GCG CAC CTG CAC GTG GAG ATC TTC GGT ACA CAG GGC AAA CCA 1254  
 Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr Gln Gly Lys Pro  
 310 315 320

GCC ATT GCC CAC CGC GAC TTC AAG AGC CGC AAT GTG CTG GTC AAG AGC 1302  
 Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val Leu Val Lys Ser  
 325 330 335 340

AAC CTG CAG TGT TGC ATC GCC GAC CTG GGC CTG GCT GTG ATG CAC TCA 1350  
 Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala Val Met His Ser  
 345 350 355

CAG GGC AGC GAT TAC CTG GAC ATC GGC AAC AAC CCG AGA GTG GGC ACC 1398  
 Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro Arg Val Gly Thr  
 360 365 370

AAG CGG TAC ATG GCA CCC GAG GTG CTG GAC GAG CAG ATC CGC ACG GAC 1446  
 Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln Ile Arg Thr Asp  
 375 380 385

TGC TTT GAG TCC TAC AAG TGG ACT GAC ATC TGG GCC TTT GGC CTG GTG 1494  
 Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala Phe Gly Leu Val  
 390 395 400

CTG TGG GAG ATT GCC CGC CGG ACC ATC GTG AAT GGC ATC GTG GAG GAC 1542  
 Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly Ile Val Glu Asp  
 405 410 415 420

TAT AGA CCA CCC TTC TAT GAT GTG GTG CCC AAT GAC CCC AGC TTT GAG 1590  
 Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp Pro Ser Phe Glu  
 425 430 435

GAC ATG AAG AAG GTG GTG TGT GTG GAT CAG CAG ACC CCC ACC ATC CCT 1638  
 Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro Thr Ile Pro  
 440 445 450

AAC CGG CTG GCT GCA GAC CCG GTC CTC TCA GGC CTA GCT CAG ATG ATG 1686  
Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala Gln Met Met  
455 460 465  
CGG GAG TGC TGG TAC CCA AAC CCC TCT GCC CGA CTC ACC GCG CTG CGG 1734  
Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg  
470 475 480  
ATC AAG AAG ACA CTA CAA AAA ATT AGC AAC AGT CCA GAG AAG CCT AAA 1782  
Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro Glu Lys Pro Lys  
485 490 495 500  
GTG ATT CAA TAGCCCAGGA GCACCTGATT CCTTTCTGCC TGCAGGGGGC 1831  
Val Ile Gln  
TGGGGGGGTG GGGGGCAGTG GATGGTGCCC TATCTGGGTA GAGGTAGTGT GAGTGTGGTG 1891  
TGTGCTGGGG ATGGGCAGCT GCGCCTGCCT GCTCGGCCCC CAGCCCACCC AGCCAAAAAT 1951  
ACAGCTGGGC TGAAACCTGA AAAAAAAAAA AAA 1984

## (2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Thr Leu Gly Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala  
1 5 10 15  
Leu Val Thr Gln Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val  
20 25 30  
Thr Cys Thr Cys Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly  
35 40 45  
Ala Trp Cys Thr Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln  
50 55 60  
Glu His Arg Gly Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg  
65 70 75 80  
Pro Thr Glu Phe Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn  
85 90 95  
His Asn Val Ser Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln  
100 105 110

Pro Gly Thr Asp Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala  
 115 120 125  
 Leu Leu Ala Leu Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg  
 130 135 140  
 Arg Arg Gln Glu Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser  
 145 150 155 160  
 Ser Leu Ile Leu Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp  
 165 170 175  
 Leu Leu Asp Ser Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe  
 180 185 190  
 Leu Val Gln Arg Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val  
 195 200 205  
 Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Leu Trp His Gly Glu  
 210 215 220  
 Ser Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe  
 225 230 235 240  
 Arg Glu Thr Glu Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile  
 245 250 255  
 Leu Gly Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln  
 260 265 270  
 Leu Trp Leu Ile Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe  
 275 280 285  
 Leu Gln Arg Gln Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val  
 290 295 300  
 Ser Ala Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr  
 305 310 315 320  
 Gln Gly Lys Pro Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val  
 325 330 335  
 Leu Val Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala  
 340 345 350  
 Val Met His Ser Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro  
 355 360 365  
 Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln  
 370 375 380  
 Ile Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala  
 385 390 395 400

Sull  
 32  
 cont

Phe Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly  
 405 410 415  
 Ile Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp  
 420 425 430  
 Pro Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr  
 435 440 445  
 Pro Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu  
 450 455 460  
 Ala Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu  
 465 470 475 480  
 Thr Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro  
 485 490 495  
 Glu Lys Pro Lys Val Ile Gln  
 500

2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 104..1630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CTCCGAGTAC CCCAGTGACC AGAGTGAGAG AAGCTCTGAA CGAGGGGCACG CGGCTTGAAG 60

GACTGTGGGC AGATGTGACC AAGAGCCTGC ATTAAGTTGT ACA ATG GTA GAT GGA 115  
 Met Val Asp Gly

GTG ATG ATT CTT CCT GTG CTT ATC ATG ATT GCT CTC CCC TCC CCT AGT 163  
 Val Met Ile Leu Pro Val Leu Ile Met Ile Ala Leu Pro Ser Pro Ser  
 5 10 15 20

ATG GAA GAT GAG AAG CCC AAG GTC AAC CCC AAA CTC TAC ATG TGT GTG 211  
 Met Glu Asp Glu Lys Pro Lys Val Asn Pro Lys Leu Tyr Met Cys Val  
 25 30 35

TGT GAA GGT CTC TCC TGC GGT AAT GAG GAC CAC TGT GAA GGC CAG CAG 259  
 Cys Glu Gly Leu Ser Cys Gly Asn Glu Asp His Cys Glu Gly Gln Gln  
 40 45 50

TGC TTT TCC TCA CTG AGC ATC AAC GAT GGC TTC CAC GTC TAC CAG AAA 307  
 Cys Phe Ser Ser Leu Ser Ile Asn Asp Gly Phe His Val Tyr Gln Lys  
 55 60 65

GGC TGC TTC CAG GTT TAT GAG CAG GGA AAG ATG ACC TGT AAG ACC CCG 355  
 Gly Cys Phe Gln Val Tyr Glu Gln Gly Lys Met Thr Cys Lys Thr Pro  
 70 75 80

CCG TCC CCT GGC CAA GCT GTG GAG TGC TGC CAA GGG GAC TGG TGT AAC 403  
 Pro Ser Pro Gly Gln Ala Val Glu Cys Cys Gln Gly Asp Trp Cys Asn  
 85 90 95 100

AGG AAC ATC ACG GCC CAG CTG CCC ACT AAA GGA AAA TCC TTC CCT GGA 451  
 Arg Asn Ile Thr Ala Gln Leu Pro Thr Lys Gly Lys Ser Phe Pro Gly  
 105 110 115

ACA CAG AAT TTC CAC TTG GAG GTT GGC CTC ATT ATT CTC TCT GTA GTG 499  
 Thr Gln Asn Phe His Leu Glu Val Gly Leu Ile Ile Leu Ser Val Val  
 120 125 130

TTC GCA GTA TGT CTT TTA GCC TGC CTG CTG GGA GTT GCT CTC CGA AAA 547  
 Phe Ala Val Cys Leu Leu Ala Cys Leu Leu Gly Val Ala Leu Arg Lys  
 135 140 145

TTT AAA AGG CGC AAC CAA GAA CGC CTC AAT CCC CGA GAC GTG GAG TAT 595  
 Phe Lys Arg Arg Asn Gln Glu Arg Leu Asn Pro Arg Asp Val Glu Tyr  
 150 155 160

GGC ACT ATC GAA GGG CTC ATC ACC ACC AAT GTT GGA GAC AGC ACT TTA 643  
 Gly Thr Ile Glu Gly Leu Ile Thr Thr Asn Val Gly Asp Ser Thr Leu  
 165 170 175 180

GCA GAT TTA TTG GAT CAT TCG TGT ACA TCA GGA AGT GGC TCT GGT CTT 691  
 Ala Asp Leu Leu Asp His Ser Cys Thr Ser Gly Ser Gly Ser Gly Leu  
 185 190 195

CCT TTT CTG GTA CAA AGA ACA GTG GCT CGC CAG ATT ACA CTG TTG GAG 739  
 Pro Phe Leu Val Gln Arg Thr Val Ala Arg Gln Ile Thr Leu Leu Glu  
 200 205 210

TGT GTC GGG AAA GGC AGG TAT GGT GAG GTG TGG AGG GGC AGC TGG CAA 787  
 Cys Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Ser Trp Gln  
 215 220 225



GGG GAA AAT GTT GCC GTG AAG ATC TTC TCC TCC CGT GAT GAG AAG TCA 835  
Gly Glu Asn Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Lys Ser  
230 235 240

TGG TTC AGG GAA ACG GAA TTG TAC AAC ACT GTG ATG CTG AGG CAT GAA 883  
Trp Phe Arg Glu Thr Glu Leu Tyr Asn Thr Val Met Leu Arg His Glu  
245 250 255 260

AAT ATC TTA GGT TTC ATT GCT TCA GAC ATG ACA TCA AGA CAC TCC AGT 931  
Asn Ile Leu Gly Phe Ile Ala Ser Asp Met Thr Ser Arg His Ser Ser  
265 270 275

ACC CAG CTG TGG TTA ATT ACA CAT TAT CAT GAA ATG GGA TCG TTG TAC 979  
Thr Gln Leu Trp Leu Ile Thr His Tyr His Glu Met Gly Ser Leu Tyr  
280 285 290

GAC TAT CTT CAG CTT ACT ACT CTG GAT ACA GTT AGC TGC CTT CGA ATA 1027  
Asp Tyr Leu Gln Leu Thr Thr Leu Asp Thr Val Ser Cys Leu Arg Ile  
295 300 305

CTG CTG TCC ATA GCT AGT GGT CTT GCA CAT TTG CAC ATA GAG ATA TTT 1075  
Val Leu Ser Ile Ala Ser Gly Leu Ala His Leu His Ile Glu Ile Phe  
310 315 320

GGG ACC CAA GGG AAA CCA GCC ATT GCC CAT CGA GAT TTA AAG AGC AAA 1123  
Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys  
325 330 335 340

AAT ATT CTG GTT AAG AAG AAT GGA CAG TGT TGC ATA GCA GAT TTG GGC 1171  
Asn Ile Leu Val Lys Lys Asn Gly Gln Cys Cys Ile Ala Asp Leu Gly  
345 350 355

CTG GCA GTC ATG CAT TCC CAG AGC ACC AAT CAG CTT GAT GTG GGG AAC 1219  
Leu Ala Val Met His Ser Gln Ser Thr Asn Gln Leu Asp Val Gly Asn  
360 365 370

AAT CCC CGT GTG GGC ACC AAG CGC TAC ATG GCC CCC GAA GTT CTA GAT 1267  
Asn Pro Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp  
375 380 385

GAA ACC ATC CAG GTG GAT TGT TTC GAT TCT TAT AAA AGG GTC GAT ATT 1315  
Glu Thr Ile Gln Val Asp Cys Phe Asp Ser Tyr Lys Arg Val Asp Ile  
390 395 400

TGG GCC TTT GGA CTT GTT TTG TGG GAA GTG GCC AGG CGG ATG GTG AGC 1363  
Trp Ala Phe Gly Leu Val Leu Trp Glu Val Ala Arg Arg Met Val Ser  
405 410 415 420

AAT GGT ATA GTG GAG GAT TAC AAG CCA CCG TTC TAC GAT GTG GTT CCC 1411  
Asn Gly Ile Val Glu Asp Tyr Lys Pro Pro Phe Tyr Asp Val Val Pro  
425 430 435

AAT GAC CCA AGT TTT GAA GAT ATG AGG AAG GTA GTC TGT GTG GAT CAA 1459  
Asn Asp Pro Ser Phe Glu Asp Met Arg Lys Val Val Cys Val Asp Gln  
440 445 450

CAA AGG CCA AAC ATA CCC AAC AGA TGG TTC TCA GAC CCG ACA TTA ACC 1507  
 Gln Arg Pro Asn Ile Pro Asn Arg Trp Phe Ser Asp Pro Thr Leu Thr  
 455 460 465

TCT CTG GCC AAG CTA ATG AAA GAA TGC TGG TAT CAA AAT CCA TCC GCA 1555  
 Ser Leu Ala Lys Leu Met Lys Glu Cys Trp Tyr Gln Asn Pro Ser Ala  
 470 475 480

AGA CTC ACA GCA CTG CGT ATC AAA AAG ACT TTG ACC AAA ATT GAT AAT 1603  
 Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Thr Lys Ile Asp Asn  
 485 490 495 500

TCC CTC GAC AAA TTG AAA ACT GAC TGT TGACATTTTC ATAGTGTCAA 1650  
 Ser Leu Asp Lys Leu Lys Thr Asp Cys  
 505

GAAGGAAGAT TTGACGTTGT TGTCATTGTC CAGCTGGGAC CTAATGCTGG CCTGACTGGT 1710

TGTCAGAATG GAATCCATCT GTCTCCCTCC CCAAATGGCT GCTTTGACAA GGCAGACGTC 1770

GTACCCAGCC ATGTGTTGGG GAGACATCAA AACCACCCTA ACCTCGCTCG ATGACTGTGA 1830

ACTGGGCATT TCACGAACTG TTCACACTGC AGAGACTAAT GTTGGACAGA CACTGTTGCA 1890

AAGGTAGGGA CTGGAGGAAC ACAGAGAAAT CCTAAAAGAG ATCTGGGCAT TAAGTCAGTG 1950

GCTTTGCATA GCTTTCACAA GTCTCCTAGA CACTCCCCAC GGGAAACTCA AGGAGGTGGT 2010

GAATTTTAA TCAGCAATAT TGCCTGTGCT TCTCTTCTTT ATTGCACTAG GAATTCTTTG 2070

CATTCCTTAC TTGCACTGTT ACTCTTAATT TTAAAGACCC AACTTGCCAA AATGTTGGCT 2130

GCGTACTCCA CTGGTCTGTC TTTGGATAAT AGGAATTCAA TTTGGCAAAA CAAAATGTAA 2190

TGTCAGACTT TGCTGCATTT TACACATGTG CTGATGTTTA CAATGATGCC GAACATTAGG 2250

AATTGTTTAT ACACAACTTT GCAAATTATT TATTACTTGT GCACTTAGTA GTTTTTACAA 2310

AACTGCTTTG TGCATATGTT AAAGCTTATT TTTATGTGGT CTTATGATTT TATTACAGAA 2370

ATGTTTTTAA CACTATACTC TAAAATGGAC ATTTTCTTTT ATTATCAGTT AAAATCACAT 2430

TTTAAGTGCT TCACATTTGT ATGTGTGTAG ACTGTAACCT TTTTTCAGTT CATATGCAGA 2490

ACGTATTTAG CCATTACCCA CGTGACACCA CCGAATATAT TATCGATTTA GAAGCAAAGA 2550

TTTCAGTAGA ATTTTAGTCC TGAACGCTAC GGGGAAAATG CATTTTCTTC AGAATTATCC 2610

ATTACGTGCA TTTAAACTCT GCCAGAAAAA AATAACTATT TTGTTTAAAT CTACTTTTGT 2670

TATTTAGTAG TTATTTGTAT AAATTAAATA AACTGTTTTT AAGTCAAAAA AAAA 2724

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Val Asp Gly Val Met Ile Leu Pro Val Leu Ile Met Ile Ala Leu  
 1 5 10 15

Pro Ser Pro Ser Met Glu Asp Glu Lys Pro Lys Val Asn Pro Lys Leu  
 20 25 30

Tyr Met Cys Val Cys Glu Gly Leu Ser Cys Gly Asn Glu Asp His Cys  
 35 40 45

Glu Gly Gln Gln Cys Phe Ser Ser Leu Ser Ile Asn Asp Gly Phe His  
 50 55 60

Val Tyr Gln Lys Gly Cys Phe Gln Val Tyr Glu Gln Gly Lys Met Thr  
 65 70 75 80

Lys Lys Thr Pro Pro Ser Pro Gly Gln Ala Val Glu Cys Cys Gln Gly  
 85 90 95

Asp Trp Cys Asn Arg Asn Ile Thr Ala Gln Leu Pro Thr Lys Gly Lys  
 100 105 110

Ser Phe Pro Gly Thr Gln Asn Phe His Leu Glu Val Gly Leu Ile Ile  
 115 120 125

Leu Ser Val Val Phe Ala Val Cys Leu Leu Ala Cys Leu Leu Gly Val  
 130 135 140

Ala Leu Arg Lys Phe Lys Arg Arg Asn Gln Glu Arg Leu Asn Pro Arg  
 145 150 155 160

Asp Val Glu Tyr Gly Thr Ile Glu Gly Leu Ile Thr Thr Asn Val Gly  
 165 170 175

Asp Ser Thr Leu Ala Asp Leu Leu Asp His Ser Cys Thr Ser Gly Ser  
 180 185 190

Gly Ser Gly Leu Pro Phe Leu Val Gln Arg Thr Val Ala Arg Gln Ile  
 195 200 205

Thr Leu Leu Glu Cys Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg  
 210 215 220

Gly Ser Trp Gln Gly Glu Asn Val Ala Val Lys Ile Phe Ser Ser Arg  
 225 230 235 240

Asp Glu Lys Ser Trp Phe Arg Glu Thr Glu Leu Tyr Asn Thr Val Met

245

250

255

Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ser Asp Met Thr Ser  
 260 265 270  
 Arg His Ser Ser Thr Gln Leu Trp Leu Ile Thr His Tyr His Glu Met  
 275 280 285  
 Gly Ser Leu Tyr Asp Tyr Leu Gln Leu Thr Thr Leu Asp Thr Val Ser  
 290 295 300  
 Cys Leu Arg Ile Val Leu Ser Ile Ala Ser Gly Leu Ala His Leu His  
 305 310 315 320  
 Ile Glu Ile Phe Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp  
 325 330 335  
 Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Gln Cys Cys Ile  
 340 345 350  
 Ala Asp Leu Gly Leu Ala Val Met His Ser Gln Ser Thr Asn Gln Leu  
 355 360 365  
 Asp Val Gly Asn Asn Pro Arg Val Gly Thr Lys Arg Tyr Met Ala Pro  
 370 375 380  
 Glu Val Leu Asp Glu Thr Ile Gln Val Asp Cys Phe Asp Ser Tyr Lys  
 385 390 395 400  
 Arg Val Asp Ile Trp Ala Phe Gly Leu Val Leu Trp Glu Val Ala Arg  
 405 410 415  
 Arg Met Val Ser Asn Gly Ile Val Glu Asp Tyr Lys Pro Pro Phe Tyr  
 420 425 430  
 Asp Val Val Pro Asn Asp Pro Ser Phe Glu Asp Met Arg Lys Val Val  
 435 440 445  
 Cys Val Asp Gln Gln Arg Pro Asn Ile Pro Asn Arg Trp Phe Ser Asp  
 450 455 460  
 Pro Thr Leu Thr Ser Leu Ala Lys Leu Met Lys Glu Cys Trp Tyr Gln  
 465 470 475 480  
 Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Thr  
 485 490 495  
 Lys Ile Asp Asn Ser Leu Asp Lys Leu Lys Thr Asp Cys  
 500 505

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2932 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 310..1905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GCTCCGCGCC GAGGGCTGGA GGATGCGTTC CCTGGGGTCC GGA~~CTT~~TATGA AAATATGCAT 60  
 CAGTTTAATA CTGTCTTGA ATT~~CA~~TGAGA TGAAGCATA GGTCAAAGCT GTTTGGAGAA 120  
 AATCAGAAGT ACAGTTTTAT CTAGCCACAT CTTGGAGGAG TCGTAAGAAA GCAGTGGGAG 180  
 TGAAGTCAT TGTCAAGTGC TTGCGATCTT TTACAAGAAA ATCTCACTGA ATGATAGTCA 240  
 TTAAATTGG TGAAGTAGCA AGACCAATTA TTAAAGGTGA CAGTACACAG GAAACATTAC 300  
 AATTGAACA ATG ACT CAG CTA TAC ATT TAC ATC AGA TTA TTG GGA GCC 348  
 Met Thr Gln Leu Tyr Ile Tyr Ile Arg Leu Leu Gly Ala  
 1 5 10  
 TAT TTG TTC ATC ATT TCT CGT GTT CAA GGA CAG AAT CTG GAT AGT ATG 396  
 Tyr Leu Phe Ile Ile Ser Arg Val Gln Gly Gln Asn Leu Asp Ser Met  
 15 20 25  
 CTT CAT GGC ACT GGG ATG AAA TCA GAC TCC GAC CAG AAA AAG TCA GAA 444  
 Leu His Gly Thr Gly Met Lys Ser Asp Ser Asp Gln Lys Lys Ser Glu  
 30 35 40 45  
 AAT GGA GTA ACC TTA GCA CCA GAG GAT ACC TTG CCT TTT TTA AAG TGC 492  
 Asn Gly Val Thr Leu Ala Pro Glu Asp Thr Leu Pro Phe Leu Lys Cys  
 50 55 60  
 TAT TGC TCA GGG CAC TGT CCA GAT GAT GCT ATT AAT AAC ACA TGC ATA 540  
 Tyr Cys Ser Gly His Cys Pro Asp Asp Ala Ile Asn Asn Thr Cys Ile  
 65 70 75  
 ACT AAT GGA CAT TGC TTT GCC ATC ATA GAA GAA GAT GAC CAG GGA GAA 588

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| Thr | Asn | Gly | His | Cys | Phe | Ala | Ile | Ile | Glu | Glu | Asp | Asp | Gln | Gly | Glu |      |  |
|     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |      |  |
| ACC | ACA | TTA | GCT | TCA | GGG | TGT | ATG | AAA | TAT | GAA | GGA | TCT | GAT | TTT | CAG | 636  |  |
| Thr | Thr | Leu | Ala | Ser | Gly | Cys | Met | Lys | Tyr | Glu | Gly | Ser | Asp | Phe | Gln |      |  |
|     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |      |  |
| TGC | AAA | GAT | TCT | CCA | AAA | GCC | CAG | CTA | CGC | CGG | ACA | ATA | GAA | TGT | TGT | 684  |  |
| Cys | Lys | Asp | Ser | Pro | Lys | Ala | Gln | Leu | Arg | Arg | Thr | Ile | Glu | Cys | Cys |      |  |
| 110 |     |     |     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |      |  |
| CGG | ACC | AAT | TTA | TGT | AAC | CAG | TAT | TTG | CAA | CCC | ACA | CTG | CCC | CCT | GTT | 732  |  |
| Arg | Thr | Asn | Leu | Cys | Asn | Gln | Tyr | Leu | Gln | Pro | Thr | Leu | Pro | Pro | Val |      |  |
|     |     |     | 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |      |  |
| GTC | ATA | GGT | CCG | TTT | TTT | GAT | GGC | AGC | ATT | CGA | TGG | CTG | GTT | TTG | CTC | 780  |  |
| Val | Ile | Gly | Pro | Phe | Phe | Asp | Gly | Ser | Ile | Arg | Trp | Leu | Val | Leu | Leu |      |  |
|     |     |     | 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |      |  |
| ATT | TCT | ATG | GCT | GTC | TGC | ATA | ATT | GCT | ATG | ATC | ATC | TTC | TCC | AGC | TGC | 828  |  |
| Gle | Ser | Met | Ala | Val | Cys | Ile | Ile | Ala | Met | Ile | Ile | Phe | Ser | Ser | Cys |      |  |
|     |     | 160 |     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |      |  |
| TTT | TGT | TAC | AAA | CAT | TAT | TGC | AAG | AGC | ATC | TCA | AGC | AGA | CGT | CGT | TAC | 876  |  |
| The | Cys | Tyr | Lys | His | Tyr | Cys | Lys | Ser | Ile | Ser | Ser | Arg | Arg | Arg | Tyr |      |  |
|     | 175 |     |     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |      |  |
| AAT | CGT | GAT | TTG | GAA | CAG | GAT | GAA | GCA | TTT | ATT | CCA | GTT | GGA | GAA | TCA | 924  |  |
| Asn | Arg | Asp | Leu | Glu | Gln | Asp | Glu | Ala | Phe | Ile | Pro | Val | Gly | Glu | Ser |      |  |
| 190 |     |     |     |     | 195 |     |     |     |     | 200 |     |     |     | 205 |     |      |  |
| GTA | AAA | GAC | CTT | ATT | GAC | CAG | TCA | CAA | AGT | TCT | GGT | AGT | GGG | TCT | GGA | 972  |  |
| Leu | Lys | Asp | Leu | Ile | Asp | Gln | Ser | Gln | Ser | Ser | Gly | Ser | Gly | Ser | Gly |      |  |
|     |     |     | 210 |     |     |     |     |     | 215 |     |     |     | 220 |     |     |      |  |
| CTA | CCT | TTA | TTG | GTT | CAG | CGA | ACT | ATT | GCC | AAA | CAG | ATT | CAG | ATG | GTC | 1020 |  |
| Leu | Pro | Leu | Leu | Val | Gln | Arg | Thr | Ile | Ala | Lys | Gln | Ile | Gln | Met | Val |      |  |
|     |     |     | 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |      |  |
| CGG | CAA | GTT | GGT | AAA | GGC | CGA | TAT | GGA | GAA | GTA | TGG | ATG | GGC | AAA | TGG | 1068 |  |
| Arg | Gln | Val | Gly | Lys | Gly | Arg | Tyr | Gly | Glu | Val | Trp | Met | Gly | Lys | Trp |      |  |
|     |     | 240 |     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |      |  |
| CGT | GGC | GAA | AAA | GTG | GCG | GTG | AAA | GTA | TTC | TTT | ACC | ACT | GAA | GAA | GCC | 1116 |  |
| Arg | Gly | Glu | Lys | Val | Ala | Val | Lys | Val | Phe | Phe | Thr | Thr | Glu | Glu | Ala |      |  |
|     | 255 |     |     |     |     | 260 |     |     |     |     | 265 |     |     |     |     |      |  |
| AGC | TGG | TTT | CGA | GAA | ACA | GAA | ATC | TAC | CAA | ACT | GTG | CTA | ATG | CGC | CAT | 1164 |  |
| Ser | Trp | Phe | Arg | Glu | Thr | Glu | Ile | Tyr | Gln | Thr | Val | Leu | Met | Arg | His |      |  |
| 270 |     |     |     |     | 275 |     |     |     |     | 280 |     |     |     | 285 |     |      |  |
| GAA | AAC | ATA | CTT | GGT | TTC | ATA | GCG | GCA | GAC | ATT | AAA | GGT | ACA | GGT | TCC | 1212 |  |
| Glu | Asn | Ile | Leu | Gly | Phe | Ile | Ala | Ala | Asp | Ile | Lys | Gly | Thr | Gly | Ser |      |  |
|     |     |     |     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |      |  |

32  
 cont.

TGG ACT CAG CTC TAT TTG ATT ACT GAT TAC CAT GAA AAT GGA TCT CTC 1260  
 Trp Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu  
 305 310 315

TAT GAC TTC CTG AAA TGT GCT ACA CTG GAC ACC AGA GCC CTG CTT AAA 1308  
 Tyr Asp Phe Leu Lys Cys Ala Thr Leu Asp Thr Arg Ala Leu Leu Lys  
 320 325 330

TTG GCT TAT TCA GCT GCC TGT GGT CTG TGC CAC CTG CAC ACA GAA ATT 1356  
 Leu Ala Tyr Ser Ala Ala Cys Gly Leu Cys His Leu His Thr Glu Ile  
 335 340 345

TAT GGC ACC CAA GGA AAG CCC GCA ATT GCT CAT CGA GAC CTA AAG AGC 1404  
 Tyr Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser  
 350 355 360 365

AAA AAC ATC CTC ATC AAG AAA AAT GGG AGT TGC TGC ATT GCT GAC CTG 1452  
 Lys Asn Ile Leu Ile Lys Lys Asn Gly Ser Cys Cys Ile Ala Asp Leu  
 370 375 380

GGC CTT GCT GTT AAA TTC AAC AGT GAC ACA AAT GAA GTT GAT GTG CCC 1500  
 Gly Leu Ala Val Lys Phe Asn Ser Asp Thr Asn Glu Val Asp Val Pro  
 385 390 395

TTG AAT ACC AGG GTG GGC ACC AAA CGC TAC ATG GCT CCC GAA GTG CTG 1548  
 Leu Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu  
 400 405 410

GAC GAA AGC CTG AAC AAA AAC CAC TTC CAG CCC TAC ATC ATG GCT GAC 1596  
 Asp Glu Ser Leu Asn Lys Asn His Phe Gln Pro Tyr Ile Met Ala Asp  
 415 420 425

ATC TAC AGC TTC GGC CTA ATC ATT TGG GAG ATG GCT CGT CGT TGT ATC 1644  
 Ile Tyr Ser Phe Gly Leu Ile Ile Trp Glu Met Ala Arg Arg Cys Ile  
 430 435 440 445

ACA GGA GGG ATC GTG GAA GAA TAC CAA TTG CCA TAT TAC AAC ATG GTA 1692  
 Thr Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr Tyr Asn Met Val  
 450 455 460

CCG AGT GAT CCG TCA TAC GAA GAT ATG CGT GAG GTT GTG TGT GTC AAA 1740  
 Pro Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys  
 465 470 475

CGT TTG CGG CCA ATT GTG TCT AAT CGG TGG AAC AGT GAT GAA TGT CTA 1788  
 Arg Leu Arg Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu  
 480 485 490

CGA GCA GTT TTG AAG CTA ATG TCA GAA TGC TGG GCC CAC AAT CCA GCC 1836  
 Arg Ala Val Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala  
 495 500 505

TCC AGA CTC ACA GCA TTG AGA ATT AAG AAG ACG CTT GCC AAG ATG GTT 1884  
 Ser Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ala Lys Met Val  
 510 515 520 525

GAA TCC CAA GAT GTA AAA ATC TGATGGTTAA ACCATCGGAG GAGAAACTCT 1935  
 Glu Ser Gln Asp Val Lys Ile  
 530

AGACTGCAAG AACTGTTTTT ACCCATGGCA TGGGTGGAAT TAGAGTGGAA TAAGGATGTT 1995  
 AACTTGGTTC TCAGACTCTT TCTTCACTAC GTGTTCACAG GCTGCTAATA TTAAACCTTT 2055  
 CAGTACTCTT ATTAGGATAC AAGCTGGGAA CTTCTAAACA CTTCATTCTT TATATATGGA 2115  
 CAGCTTTATT TTAAATGTGG TTTTGTATGC CTTTTTTTAA GTGGGTTTTT ATGAACTGCA 2175  
 TCAAGACTTC AATCCTGATT AGTGTCTCCA GTCAAGCTCT GGGTACTGAA TTGCCTGTTC 2235  
 ATAAAACGGT GCTTCTGTG AAAGCCTTAA GAAGATAAAT GAGCGCAGCA GAGATGGAGA 2295  
 AATAGACTTT GCCTTTTACC TGAGACATTC AGTTCGTTTG TATTCTACCT TTGTAAAACA 2355  
 GCCTATAGAT GATGATGTGT TTGGGATACT GCTTATTTTA TGATAGTTTG TCCTGTGTCC 2415  
 TTAGTGATGT GTGTGTGTCT CCATGCACAT GCACGCCGGG ATTCCTCTGC TGCCATTTGA 2475  
 ATTAGAAGAA AATAATTTAT ATGCATGCAC AGGAAGATAT TGGTGGCCGG TGGTTTTGTG 2535  
 GTTTAAAAAT GCAATATCTG ACCAAGATTC GCCAATCTCA TACAAGCCAT TTAAGTTGCA 2595  
 AGTGAGATAG CTTCCCCACC AGCTTTATTT TTTAACATGA AAGCTGATGC CAAGGCCAAA 2655  
 AGAAGTTTAA AGCATCTGTA AATTTGGACT GTTTTCCTTC AACCACCATT TTTTTTGTGG 2715  
 TTATTATTTT TGTCACGGAA AGCATCCTCT CCAAGTTGG AGCTTCTATT GCCATGAACC 2775  
 ATGCTTACAA AGAAAGCACT TCTTATTGAA GTGAATTCCT GCATTTGATA GCAATGTAAG 2835  
 TGCCTATAAC CATGTTCTAT ATTCTTTATT CTCAGTAACT TTTAAAGGG AAGTTATTTA 2895  
 TATTTTGTGT ATAATGTGCT TTATTTGCAA ATCACCC 2932

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 532 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Thr Gln Leu Tyr Ile Tyr Ile Arg Leu Leu Gly Ala Tyr Leu Phe  
 1 5 10 15  
 Ile Ile Ser Arg Val Gln Gly Gln Asn Leu Asp Ser Met Leu His Gly  
 20 25 30



Thr Gly Met Lys Ser Asp Ser Asp Gln Lys Lys Ser Glu Asn Gly Val  
 35 40 45  
 Thr Leu Ala Pro Glu Asp Thr Leu Pro Phe Leu Lys Cys Tyr Cys Ser  
 50 55 60  
 Gly His Cys Pro Asp Asp Ala Ile Asn Asn Thr Cys Ile Thr Asn Gly  
 65 70 75 80  
 His Cys Phe Ala Ile Ile Glu Glu Asp Asp Gln Gly Glu Thr Thr Leu  
 85 90 95  
 Ala Ser Gly Cys Met Lys Tyr Glu Gly Ser Asp Phe Gln Cys Lys Asp  
 100 105 110  
 Ser Pro Lys Ala Gln Leu Arg Arg Thr Ile Glu Cys Cys Arg Thr Asn  
 115 120 125  
 Leu Cys Asn Gln Tyr Leu Gln Pro Thr Leu Pro Pro Val Val Ile Gly  
 130 135 140  
 Pro Phe Phe Asp Gly Ser Ile Arg Trp Leu Val Leu Leu Ile Ser Met  
 145 150 155 160  
 Ala Val Cys Ile Ile Ala Met Ile Ile Phe Ser Ser Cys Phe Cys Tyr  
 165 170 175  
 Lys His Tyr Cys Lys Ser Ile Ser Ser Arg Arg Arg Tyr Asn Arg Asp  
 180 185 190  
 Leu Glu Gln Asp Glu Ala Phe Ile Pro Val Gly Glu Ser Leu Lys Asp  
 195 200 205  
 Leu Ile Asp Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly Leu Pro Leu  
 210 215 220  
 Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val Arg Gln Val  
 225 230 235 240  
 Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp Arg Gly Glu  
 245 250 255  
 Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala Ser Trp Phe  
 260 265 270  
 Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His Glu Asn Ile  
 275 280 285  
 Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser Trp Thr Gln  
 290 295 300  
 Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu Tyr Asp Phe  
 305 310 315 320  
 Leu Lys Cys Ala Thr Leu Asp Thr Arg Ala Leu Leu Lys Leu Ala Tyr

Ser  
 32  
 cont

325

330

335

Ser Ala Ala Cys Gly Leu Cys His Leu His Thr Glu Ile Tyr Gly Thr  
 340 345 350  
 Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys Asn Ile  
 355 360 365  
 Leu Ile Lys Lys Asn Gly Ser Cys Cys Ile Ala Asp Leu Gly Leu Ala  
 370 375 380  
 Val Lys Phe Asn Ser Asp Thr Asn Glu Val Asp Val Pro Leu Asn Thr  
 385 390 395 400  
 Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Ser  
 405 410 415  
 Leu Asn Lys Asn His Phe Gln Pro Tyr Ile Met Ala Asp Ile Tyr Ser  
 420 425 430  
 Phe Gly Leu Ile Ile Trp Glu Met Ala Arg Arg Cys Ile Thr Gly Gly  
 435 440 445  
 Ile Val Glu Glu Tyr Gln Leu Pro Tyr Tyr Asn Met Val Pro Ser Asp  
 450 455 460  
 Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys Arg Leu Arg  
 465 470 475 480  
 Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu Arg Ala Val  
 485 490 495  
 Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala Ser Arg Leu  
 500 505 510  
 Thr Ala Leu Arg Ile Lys Lys Thr Leu Ala Lys Met Val Glu Ser Gln  
 515 520 525  
 Asp Val Lys Ile  
 530

12) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1515

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

|   |     |
|---|-----|
| ATG GCG GAG TCG GCC GGA GCC TCC TCC TTC TTC CCC CTT GTT GTC CTC | 48  |
| Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu Val Val Leu |     |
| 1 5 10 15   |     |
| CTG CTC GCC GGC AGC GGC GGG TCC GGG CCC CGG GGG GTC CAG GCT CTG | 96  |
| Leu Leu Ala Gly Ser Gly Gly Ser Gly Pro Arg Gly Val Gln Ala Leu |     |
| 20 25 30  |     |
| GTG TGT GCG TGC ACC AGC TGC CTC CAG GCC AAC TAC ACG TGT GAG ACA | 144 |
| Leu Cys Ala Cys Thr Ser Cys Leu Gln Ala Asn Tyr Thr Cys Glu Thr |     |
| 35 40 45  |     |
| GAT GGG GCC TGC ATG GTT TCC TTT TTC AAT CTG GAT GGG ATG GAG CAC | 192 |
| Asp Gly Ala Cys Met Val Ser Phe Phe Asn Leu Asp Gly Met Glu His |     |
| 50 55 60  |     |
| GAT GTG CGC ACC TGC ATC CCC AAA GTG GAG CTG GTC CCT GCC GGG AAG | 240 |
| As Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro Ala Gly Lys  |     |
| 65 70 75 80   |     |
| CCC TTC TAC TGC CTG AGC TCG GAG GAC CTG CGC AAC ACC CAC TGC TGC | 288 |
| Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr His Cys Cys |     |
| 85 90 95  |     |
| TAC ACT GAC TAC TGC AAC AGG ATC GAC TTG AGG GTG CCC AGT GGT CAC | 336 |
| Tyr Thr Asp Tyr Cys Asn Arg Ile Asp Leu Arg Val Pro Ser Gly His |     |
| 100 105 110   |     |
| CTC AAG GAG CCT GAG CAC CCG TCC ATG TGG GGC CCG GTG GAG CTG GTA | 384 |
| Leu Lys Glu Pro Glu His Pro Ser Met Trp Gly Pro Val Glu Leu Val |     |
| 115 120 125   |     |
| GGC ATC ATC GCC GGC CCG GTG TTC CTC CTG TTC CTC ATC ATC ATC ATT | 432 |
| Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile Ile Ile Ile |     |
| 130 135 140   |     |
| GTT TTC CTT GTC ATT AAC TAT CAT CAG CGT GTC TAT CAC AAC CGC CAG | 480 |
| Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His Asn Arg Gln |     |
| 145 150 155 160   |     |
| AGA CTG GAC ATG GAA GAT CCC TCA TGT GAG ATG TGT CTC TCC AAA GAC | 528 |
| Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met Cys Leu Ser Lys Asp |     |
| 165 170 175   |     |

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|   |      |
|---|------|
| AAG ACC CTC CAG GAT CTT GTC TAC GAT CTC TCC ACC TCA GGG TCT GGC | 576  |
| Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser Thr Ser Gly Ser Gly |      |
| 180 185 190   |      |
| TCA GGG TTA CCC CTC TTT GTC CAG CGC ACA GTG GCC CGA ACC ATC GTT | 624  |
| Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val Ala Arg Thr Ile Val |      |
| 195 200 205   |      |
| TTA CAA GAG ATT ATT GGC AAG GGT CGG TTT GGG GAA GTA TGG CGG GGC | 672  |
| Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe Gly Glu Val Trp Arg Gly |      |
| 210 215 220   |      |
| CGC TGG AGG GGT GGT GAT GTG GCT GTG AAA ATA TTC TCT TCT CGT GAA | 720  |
| Arg Trp Arg Gly Gly Asp Val Ala Val Lys Ile Phe Ser Ser Arg Glu |      |
| 225 230 235 240   |      |
| GAA CGG TCT TGG TTC AGG GAA GCA GAG ATA TAC CAG ACG GTC ATG CTG | 768  |
| Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr Val Met Leu |      |
| 245 250 255   |      |
| CGC CAT GAA AAC ATC CTT CGA TTT ATT GCT GCT GAC AAT AAA GAT AAT | 816  |
| Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn Lys Asp Asn |      |
| 260 265 270   |      |
| GGC ACC TGG ACA CAG CTG TGG CTT GTT TCT GAC TAT CAT GAG CAC GGG | 864  |
| Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His Glu His Gly |      |
| 275 280 285   |      |
| TCC CTG TTT GAT TAT CTG AAC CGG TAC ACA GTG ACA ATT GAG GGG ATG | 912  |
| Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Ile Glu Gly Met |      |
| 290 295 300   |      |
| ATT AAG CTG GCC TTG TCT GCT GCT AGT GGG CTG GCA CAC CTG CAC ATG | 960  |
| Ile Lys Leu Ala Leu Ser Ala Ala Ser Gly Leu Ala His Leu His Met |      |
| 305 310 315 320   |      |
| GAG ATC GTG GGC ACC CAA GGG AAG CCT GCA ATT GCT CAT CGA GAC TTA | 1008 |
| Glu Ile Val Gly Thr Gln Gly Lys Pro Gly Ile Ala His Arg Asp Leu |      |
| 325 330 335   |      |
| AAG TCA AAG AAC ATT CTG GTG AAG AAA AAT GGC ATG TGT GCC ATA GCA | 1056 |
| Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Met Cys Ala Ile Ala |      |
| 340 345 350   |      |
| GAC CTG GGC CTG GCT GTC CGT CAT GAT GCA GTC ACT GAC ACC ATT GAC | 1104 |
| Asp Leu Gly Leu Ala Val Arg His Asp Ala Val Thr Asp Thr Ile Asp |      |
| 355 360 365   |      |
| ATT GCC CCG AAT CAG AGG GTG GGG ACC AAA CGA TAC ATG GCC CCT GAA | 1152 |
| Ile Ala Pro Asn Gln Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu |      |
| 370 375 380   |      |
| GTA CTT GAT GAA ACC ATT AAT ATG AAA CAC TTT GAC TCC TTT AAA TGT | 1200 |
| Val Leu Asp Glu Thr Ile Asn Met Lys His Phe Asp Ser Phe Lys Cys |      |

385 390 395 400

GCT GAT ATT TAT GCC CTC GGG CTT GTA TAT TGG GAG ATT GCT CGA AGA 1248  
 Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp Glu Ile Ala Arg Arg  
 405 410 415

TGC AAT TCT GGA GGA GTC CAT GAA GAA TAT CAG CTG CCA TAT TAC GAC 1296  
 Cys Asn Ser Gly Gly Val His Glu Glu Tyr Gln Leu Pro Tyr Tyr Asp  
 420 425 430

TTA GTG CCC TCT GAC CCT TCC ATT GAG GAA ATG CGA AAG GTT GTA TGT 1344  
 Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg Lys Val Val Cys  
 435 440 445

GAT CAG AAG CTG CGT CCC AAC ATC CCC AAC TGG TGG CAG AGT TAT GAG 1392  
 Asp Gln Lys Leu Arg Pro Asn Ile Pro Asn Trp Trp Gln Ser Tyr Glu  
 450 455 460

GCA CTG CGG GTG ATG GGG AAG ATG ATG CGA GAG TGT TGG TAT GCC AAC 1440  
 Ala Leu Arg Val Met Gly Lys Met Met Arg Glu Cys Trp Tyr Ala Asn  
 465 470 475 480

GGC GCA GCC CGC CTG ACG GCC CTG CGC ATC AAG AAG ACC CTC TCC CAG 1488  
 Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln  
 485 490 495

CTC AGC GTG CAG GAA GAC GTG AAG ATC TAACTGCTCC CTCTCTCCAC 1535  
 Leu Ser Val Gln Glu Asp Val Lys Ile  
 500 505

ACGGAGCTCC TGGCAGCGAG AACTACGCAC AGCTGCCGCG TTGAGCGTAC GATGGAGGCC 1595

TACCTCTCGT TTCTGCCCAG CCCTCTGTGG CCAGGAGCCC TGGCCCGCAA GAGGGACAGA 1655

GCCCGGGAGA GACTCGCTCA CTCCCATGTT GGGTTTGAGA CAGACACCTT TTCTATTTAC 1715

CTCCTAATGG CATGGAGACT CTGAGAGCGA ATTGTGTGGA GAACTCAGTG CCACACCTCG 1775

AACTGGTTGT AGTGGAAGT CCCGCGAAAC CCGGTGCATC TGGCACGTGG CCAGGAGCCA 1835

TGACAGGGGC GCTTGGGAGG GGCCGGAGGA ACCGAGGTGT TGCCAGTGCT AAGCTGCCCT 1895

GAGGGTTTCC TTCGGGGACC AGCCCACAGC ACACCAAGGT GGCCCGGAAG AACCAGAAGT 1955

GCAGCCCCTC TCACAGGCAG CTCTGAGCCG CGCTTTCCCC TCCTCCCTGG GATGGACGCT 2015

GCCGGGAGAC TGCCAGTGGA GACGGAATCT GCCGCTTTGT CTGTCCAGCC GTGTGTGCAT 2075

GTGCCGAGGT GCGTCCCCCG TTGTGCCTGG TTCGTGCCAT GCCCTTACAC GTGCGTGTGA 2135

GTGTGTGTGT GTGTCTGTAG GTGCGCACTT ACCTGCTTGA GCTTTCTGTG CATGTGCAGG 2195

TCGGGGGTGT GGTCGTCATG CTGTCCGTGC TTGCTGGTGC CTCTTTTCAG TAGTGAGCAG 2255

CATCTAGTTT CCCTGGTGCC CTTCCCTGGA GGTCTCTCCC TCCCCAGAG CCCCTCATGC 2315

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32  
cont

CACAGTGGTA CTCTGTGT

## (2) INFORMATION FOR SEQ ID NO: 8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu Val Val Leu  
 1 5 10 15  
 Leu Leu Ala Gly Ser Gly Gly Ser Gly Pro Arg Gly Val Gln Ala Leu  
 20 25 30  
 Leu Cys Ala Cys Thr Ser Cys Leu Gln Ala Asn Tyr Thr Cys Glu Thr  
 35 40 45  
 Asp Gly Ala Cys Met Val Ser Phe Phe Asn Leu Asp Gly Met Glu His  
 50 55 60  
 His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro Ala Gly Lys  
 65 70 75 80  
 Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr His Cys Cys  
 85 90 95  
 Tyr Thr Asp Tyr Cys Asn Arg Ile Asp Leu Arg Val Pro Ser Gly His  
 100 105 110  
 Leu Lys Glu Pro Glu His Pro Ser Met Trp Gly Pro Val Glu Leu Val  
 115 120 125  
 Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile Ile Ile Ile  
 130 135 140  
 Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His Asn Arg Gln  
 145 150 155 160  
 Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met Cys Leu Ser Lys Asp  
 165 170 175  
 Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser Thr Ser Gly Ser Gly  
 180 185 190  
 Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val Ala Arg Thr Ile Val  
 195 200 205  
 Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe Gly Glu Val Trp Arg Gly

Sub  
 32  
 cont

| 210        |            |            |            |            | 215        |            |            |            |            | 220        |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Arg<br>225 | Trp        | Arg        | Gly        | Gly        | Asp<br>230 | Val        | Ala        | Val        | Lys        | Ile<br>235 | Phe        | Ser        | Ser        | Arg        | Glu<br>240 |
| Glu        | Arg        | Ser        | Trp        | Phe<br>245 | Arg        | Glu        | Ala        | Glu        | Ile<br>250 | Tyr        | Gln        | Thr        | Val        | Met<br>255 | Leu        |
| Arg        | His        | Glu        | Asn<br>260 | Ile        | Leu        | Gly        | Phe        | Ile<br>265 | Ala        | Ala        | Asp        | Asn        | Lys<br>270 | Asp        | Asn        |
| Gly        | Thr        | Trp<br>275 | Thr        | Gln        | Leu        | Trp        | Leu<br>280 | Val        | Ser        | Asp        | Tyr        | His<br>285 | Glu        | His        | Gly        |
| Ser        | Leu<br>290 | Phe        | Asp        | Tyr        | Leu        | Asn<br>295 | Arg        | Tyr        | Thr        | Val        | Thr<br>300 | Ile        | Glu        | Gly        | Met        |
| Ile<br>305 | Lys        | Leu        | Ala        | Leu        | Ser<br>310 | Ala        | Ala        | Ser        | Gly        | Leu<br>315 | Ala        | His        | Leu        | His        | Met<br>320 |
| Glu        | Ile        | Val        | Gly        | Thr<br>325 | Gln        | Gly        | Lys        | Pro        | Gly<br>330 | Ile        | Ala        | His        | Arg        | Asp<br>335 | Leu        |
| Lys        | Ser        | Lys        | Asn<br>340 | Ile        | Leu        | Val        | Lys        | Lys<br>345 | Asn        | Gly        | Met        | Cys        | Ala<br>350 | Ile        | Ala        |
| Asp        | Leu        | Gly<br>355 | Leu        | Ala        | Val        | Arg        | His<br>360 | Asp        | Ala        | Val        | Thr        | Asp<br>365 | Thr        | Ile        | Asp        |
| Ile<br>370 | Ala        | Pro        | Asn        | Gln        | Arg        | Val<br>375 | Gly        | Thr        | Lys        | Arg        | Tyr<br>380 | Met        | Ala        | Pro        | Glu        |
| Val<br>385 | Leu        | Asp        | Glu        | Thr        | Ile<br>390 | Asn        | Met        | Lys        | His        | Phe<br>395 | Asp        | Ser        | Phe        | Lys        | Cys<br>400 |
| Ala        | Asp        | Ile        | Tyr        | Ala<br>405 | Leu        | Gly        | Leu        | Val<br>410 | Tyr        | Trp        | Glu        | Ile        | Ala        | Arg<br>415 | Arg        |
| Cys        | Asn        | Ser        | Gly<br>420 | Gly        | Val        | His        | Glu        | Glu<br>425 | Tyr        | Gln        | Leu        | Pro        | Tyr<br>430 | Tyr        | Asp        |
| Leu        | Val<br>435 | Pro        | Ser        | Asp        | Pro        | Ser        | Ile<br>440 | Glu        | Glu        | Met        | Arg        | Lys<br>445 | Val        | Val        | Cys        |
| Asp<br>450 | Gln        | Lys        | Leu        | Arg        | Pro        | Asn<br>455 | Ile        | Pro        | Asn        | Trp<br>460 | Trp        | Gln        | Ser        | Tyr        | Glu        |
| Ala<br>465 | Leu        | Arg        | Val        | Met        | Gly<br>470 | Lys        | Met        | Met        | Arg        | Glu<br>475 | Cys        | Trp        | Tyr        | Ala        | Asn<br>480 |
| Gly        | Ala        | Ala        | Arg        | Leu<br>485 | Thr        | Ala        | Leu        | Arg        | Ile<br>490 | Lys        | Lys        | Thr        | Leu        | Ser<br>495 | Gln        |
| Leu        | Ser        | Val        | Gln        | Glu        | Asp        | Val        | Lys        | Ile<br>500 |            |            |            |            |            |            |            |

Seq  
32  
cont

## (2) INFORMATION FOR SEQ ID NO: 9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 77..1585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GCGGAGGCGA GGTTTGCTGG GGTGAGGCAG CGGCGCGGCC GGGCCGGGCC GGGCCACAGG 60  
 GGTGGCGGC GGGACC ATG GAG GCG GCG GTC GCT GCT CCG CGT CCC CGG 109  
 Met Glu Ala Ala Val Ala Ala Pro Arg Pro Arg  
 1 5 10  
 CTG CTC CTC CTC GTG CTG GCG GCG GCG GCG GCG GCG GCG GCG GCG CTG 157  
 Leu Leu Leu Leu Val Leu Ala Ala Ala Ala Ala Ala Ala Ala Leu  
 15 20 25  
 CTC CCG GGG GCG ACG GCG TTA CAG TGT TTC TGC CAC CTC TGT ACA AAA 205  
 Leu Pro Gly Ala Thr Ala Leu Gln Cys Phe Cys His Leu Cys Thr Lys  
 30 35 40  
 GAC AAT TTT ACT TGT GTG ACA GAT GGG CTC TGC TTT GTC TCT GTC ACA 253  
 Asp Asn Phe Thr Cys Val Thr Asp Gly Leu Cys Phe Val Ser Val Thr  
 45 50 55  
 GAG ACC ACA GAC AAA GTT ATA CAC AAC AGC ATG TGT ATA GCT GAA ATT 301  
 Glu Thr Thr Asp Lys Val Ile His Asn Ser Met Cys Ile Ala Glu Ile  
 60 65 70 75  
 GAC TTA ATT CCT CGA GAT AGG CCG TTT GTA TGT GCA CCC TCT TCA AAA 349  
 Asp Leu Ile Pro Arg Asp Arg Pro Phe Val Cys Ala Pro Ser Ser Lys  
 80 85 90  
 ACT GGG TCT GTG ACT ACA ACA TAT TGC TGC AAT CAG GAC CAT TGC AAT 397  
 Thr Gly Ser Val Thr Thr Thr Tyr Cys Cys Asn Gln Asp His Cys Asn



95

100

105

AAA ATA GAA CTT CCA ACT ACT GTA AAG TCA TCA CCT GGC CTT GGT CCT 445  
 Lys Ile Glu Leu Pro Thr Thr Val Lys Ser Ser Pro Gly Leu Gly Pro  
 110 115 120

GTG GAA CTG GCA GCT GTC ATT GCT GGA CCA GTG TGC TTC GTC TGC ATC 493  
 Val Glu Leu Ala Ala Val Ile Ala Gly Pro Val Cys Phe Val Cys Ile  
 125 130 135

TCA CTC ATG TTG ATG GTC TAT ATC TGC CAC AAC CGC ACT GTC ATT CAC 541  
 Ser Leu Met Leu Met Val Tyr Ile Cys His Asn Arg Thr Val Ile His  
 140 145 150 155

CAT CGA GTG CCA AAT GAA GAG GAC CCT TCA TTA GAT CGC CCT TTT ATT 589  
 His Arg Val Pro Asn Glu Glu Asp Pro Ser Leu Asp Arg Pro Phe Ile  
 160 165 170

TCA GAG GGT ACT ACG TTG AAA GAC TTA ATT TAT GAT ATG ACA ACG TCA 637  
 Ser Glu Gly Thr Thr Leu Lys Asp Leu Ile Tyr Asp Met Thr Thr Ser  
 175 180 185

GGT TCT GGC TCA GGT TTA CCA TTG CTT GTT CAG AGA ACA ATT GCG AGA 685  
 Gly Ser Gly Ser Gly Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Arg  
 190 195 200

ACT ATT GTG TTA CAA GAA AGC ATT GGC AAA GGT CGA TTT GGA GAA GTT 733  
 Thr Ile Val Leu Gln Glu Ser Ile Gly Lys Gly Arg Phe Gly Glu Val  
 205 210 215

TGG AGA GGA AAG TGG CGG GGA GAA GAA GTT GCT GTT AAG ATA TTC TCC 781  
 Trp Arg Gly Lys Trp Arg Gly Glu Glu Val Ala Val Lys Ile Phe Ser  
 220 225 230 235

TCT AGA GAA GAA CGT TCG TGG TTC CGT GAG GCA GAG ATT TAT CAA ACT 829  
 Ser Arg Glu Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr  
 240 245 250

GTA ATG TTA CGT CAT GAA AAC ATC CTG GGA TTT ATA GCA GCA GAC AAT 877  
 Val Met Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn  
 255 260 265

AAA GAC AAT GGT ACT TGG ACT CAG CTC TGG TTG GTG TCA GAT TAT CAT 925  
 Lys Asp Asn Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His  
 270 275 280

GAG CAT GGA TCC CTT TTT GAT TAC TTA AAC AGA TAC ACA GTT ACT GTG 973  
 Glu His Gly Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Val  
 285 290 295

GAA GGA ATG ATA AAA CTT GCT CTG TCC ACG GCG AGC GGT CTT GCC CAT 1021  
 Glu Gly Met Ile Lys Leu Ala Leu Ser Thr Ala Ser Gly Leu Ala His  
 300 305 310 315

CTT CAC ATG GAG ATT GTT GGT ACC CAA GGA AAG CCA GCC ATT GCT CAT 1069

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 32  
 cont

Leu His Met Glu Ile Val Gly Thr Gln Gly Lys Pro Ala Ile Ala His  
 320 325 330

AGA GAT TTG AAA TCA AAG AAT ATC TTG GTA AAG AAG AAT GGA ACT TGC 1117  
 Arg Asp Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Thr Cys  
 335 340 345

TGT ATT GCA GAC TTA GGA CTG GCA GTA AGA CAT GAT TCA GCC ACA GAT 1165  
 Cys Ile Ala Asp Leu Gly Leu Ala Val Arg His Asp Ser Ala Thr Asp  
 350 355 360

ACC ATT GAT ATT GCT CCA AAC CAC AGA GTG GGA ACA AAA AGG TAC ATG 1213  
 Thr Ile Asp Ile Ala Pro Asn His Arg Val Gly Thr Lys Arg Tyr Met  
 365 370 375

GCC CCT GAA GTT CTC GAT GAT TCC ATA AAT ATG AAA CAT TTT GAA TCC 1261  
 Ala Pro Glu Val Leu Asp Asp Ser Ile Asn Met Lys His Phe Glu Ser  
 380 385 390 395

TTC AAA CGT GCT GAC ATC TAT GCA ATG GGC TTA GTA TTC TGG GAA ATT 1309  
 Phe Lys Arg Ala Asp Ile Tyr Ala Met Gly Leu Val Phe Trp Glu Ile  
 400 405 410

GGT CGA CGA TGT TCC ATT GGT GGA ATT CAT GAA GAT TAC CAA CTG CCT 1357  
 Ala Arg Arg Cys Ser Ile Gly Gly Ile His Glu Asp Tyr Gln Leu Pro  
 415 420 425

TAT TAT GAT CTT GTA CCT TCT GAC CCA TCA GTT GAA GAA ATG AGA AAA 1405  
 Tyr Tyr Asp Leu Val Pro Ser Asp Pro Ser Val Glu Glu Met Arg Lys  
 430 435 440

GTT GTT TGT GAA CAG AAG TTA AGG CCA AAT ATC CCA AAC AGA TGG CAG 1453  
 Val Val Cys Glu Gln Lys Leu Arg Pro Asn Ile Pro Asn Arg Trp Gln  
 445 450 455

AGC TGT GAA GCC TTG AGA GTA ATG GGT AAA ATT ATG AGA GAA TGT TGG 1501  
 Ser Cys Glu Ala Leu Arg Val Met Ala Lys Ile Met Arg Glu Cys Trp  
 460 465 470 475

TAT GCC AAT GGA GCA GCT AGG CTT ACA GCA TTG CGG ATT AAG AAA ACA 1549  
 Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr  
 480 485 490

TTA TCG CAA CTC AGT CAA CAG GAA GGC ATC AAA ATG TAATTCTACA 1595  
 Leu Ser Gln Leu Ser Gln Gln Glu Gly Ile Lys Met  
 495 500

GCTTTGCCTG AACTCTCCTT TTTTCTTCAG ATCTGCTCCT GGGTTTAAAT TTGGGAGGTC 1655

AGTTGTTCTA CCTCACTGAG AGGGAACAGA AGGATATTGC TTCCTTTTGC AGCAGTGTA 1715

TAAAGTCAAT TAAAACTTC CCAGGATTTC TTTGGACCCA GAAACAGCC ATGTGGGTCC 1775

TTTCTGTGCA CTATGAACGC TTCTTTCCCA GGACAGAAAA TGTTAGTCT ACCTTTATTT 1835

TTTATTAACA AACTTGTTT TTTAAAAAGA TGATTGCTGG TCTTAACTTT AGGTAAGTCT 1895  
 GCTGTGCTGG AGATCATCTT TAAGGGCAAA GGAGTTGGAT TGCTGAATTA CAATGAAACA 1955  
 TGTCTTATTA CTAAAGAAAG TGATTTACTC CTGGTTAGTA CATTCTCAGA GGATTCTGAA 2015  
 CCACTAGAGT TTCCTTGATT CAGACTTTGA ATGTAAGTGT CTATAGTTTT TCAGGATCTT 2075  
 AAAACTAACA CTTATAAAAC TCTTATCTTG AGTCTAAAAA TGACCTCATA TAGTAGTGAG 2135  
 GAACATAATT CATGCAATTG TATTTTGTAT ACTATTATTG TTCTTTCACT TATTCAGAAC 2195  
 ATTACATGCC TTCAAAATGG GATTGTACTA TACCAGTAAG TGCCACTTCT GTGTCTTTCT 2255  
 AATGGAAATG AGTAGAATTG CTGAAAGTCT CTATGTTAAA ACCTATAGTG TTT 2308

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Glu Ala Ala Val Ala Ala Pro Arg Pro Arg Leu Leu Leu Leu Val  
 5 10 15  
 Leu Ala Ala Ala Ala Ala Ala Ala Ala Leu Leu Pro Gly Ala Thr  
 20 25 30  
 Ala Leu Gln Cys Phe Cys His Leu Cys Thr Lys Asp Asn Phe Thr Cys  
 35 40 45  
 Val Thr Asp Gly Leu Cys Phe Val Ser Val Thr Glu Thr Thr Asp Lys  
 50 55 60  
 Val Ile His Asn Ser Met Cys Ile Ala Glu Ile Asp Leu Ile Pro Arg  
 65 70 75 80  
 Asp Arg Pro Phe Val Cys Ala Pro Ser Ser Lys Thr Gly Ser Val Thr  
 85 90 95  
 Thr Thr Tyr Cys Cys Asn Gln Asp His Cys Asn Lys Ile Glu Leu Pro  
 100 105 110  
 Thr Thr Val Lys Ser Ser Pro Gly Leu Gly Pro Val Glu Leu Ala Ala  
 115 120 125  
 Val Ile Ala Gly Pro Val Cys Phe Val Cys Ile Ser Leu Met Leu Met  
 130 135 140

Val Tyr Ile Cys His Asn Arg Thr Val Ile His His Arg Val Pro Asn  
 145 150 155 160  
 Glu Glu Asp Pro Ser Leu Asp Arg Pro Phe Ile Ser Glu Gly Thr Thr  
 165 170 175  
 Leu Lys Asp Leu Ile Tyr Asp Met Thr Thr Ser Gly Ser Gly Ser Gly  
 180 185 190  
 Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Arg Thr Ile Val Leu Gln  
 195 200 205  
 Glu Ser Ile Gly Lys Gly Arg Phe Gly Glu Val Trp Arg Gly Lys Trp  
 210 215 220  
 Arg Gly Glu Glu Val Ala Val Lys Ile Phe Ser Ser Arg Glu Glu Arg  
 225 230 235 240  
 Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr Val Met Leu Arg His  
 245 250 255  
 Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn Lys Asp Asn Gly Thr  
 260 265 270  
 Thr Thr Gln Leu Trp Leu Val Ser Asp Tyr His Glu His Gly Ser Leu  
 275 280 285  
 Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Val Glu Gly Met Ile Lys  
 290 295 300  
 Leu Ala Leu Ser Thr Ala Ser Gly Leu Ala His Leu His Met Glu Ile  
 305 310 315 320  
 Val Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser  
 325 330 335  
 Lys Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp Leu  
 340 345 350  
 Gly Leu Ala Val Arg His Asp Ser Ala Thr Asp Thr Ile Asp Ile Ala  
 355 360 365  
 Pro Asn His Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu  
 370 375 380  
 Asp Asp Ser Ile Asn Met Lys His Phe Glu Ser Phe Lys Arg Ala Asp  
 385 390 395 400  
 Ile Tyr Ala Met Gly Leu Val Phe Trp Glu Ile Ala Arg Arg Cys Ser  
 405 410 415  
 Ile Gly Gly Ile His Glu Asp Tyr Gln Leu Pro Tyr Tyr Asp Leu Val  
 420 425 430  
 Pro Ser Asp Pro Ser Val Glu Glu Met Arg Lys Val Val Cys Glu Gln

full  
 52  
 ant

435                                      440                                      445  
 Lys Leu Arg Pro Asn Ile Pro Asn Arg Trp Gln Ser Cys Glu Ala Leu  
 450                                      455                                      460  
 Arg Val Met Ala Lys Ile Met Arg Glu Cys Trp Tyr Ala Asn Gly Ala  
 465                                      470                                      475                                      480  
 Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln Leu Ser  
 485                                      490                                      495  
 Gln Gln Glu Gly Ile Lys Met  
 500

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1922 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 241..1746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GAGAGCACAG CCCTTCCCAG TCCCCGGAGC CGCCGCGGCA CGCGCGCATG ATCAAGACCT 60  
 TTTCCCCGGC CCCACAGGGC CTCTGGACGT GAGACCCCGG CCGCCTCCGC AAGGAGAGGC 120  
 GGGGGTCGAG TCGCCCTGTC CAAAGGCCTC AATCTAAACA ATCTTGATTG CTGTTGCCGG 180  
 CTGGCGGGAC CCTGAATGGC AGGAAATCTC ACCACATCTC TTCTCCTATC TCCAAGGACC 240  
 ATG ACC TTG GGG AGC TTC AGA AGG GGC CTT TTG ATG CTG TCG GTG GCC 288  
 Met Thr Leu Gly Ser Phe Arg Arg Gly Leu Leu Met Leu Ser Val Ala  
 1                                      5                                      10                                      15  
 TTG GGC CTA ACC CAG GGG AGA CTT GCG AAG CCT TCC AAG CTG GTG AAC 336  
 Leu Gly Leu Thr Gln Gly Arg Leu Ala Lys Pro Ser Lys Leu Val Asn

20

25

30

TGC ACT TGT GAG AGC CCA CAC TGC AAG AGA CCA TTC TGC CAG GGG TCA 384  
 Cys Thr Cys Glu Ser Pro His Cys Lys Arg Pro Phe Cys Gln Gly Ser  
 35 40 45

TGG TGC ACA GTG GTG CTG GTT CGA GAG CAG GGC AGG CAC CCC CAG GTC 432  
 Trp Cys Thr Val Val Leu Val Arg Glu Gln Gly Arg His Pro Gln Val  
 50 55 60

TAT CGG GGC TGT GGG AGC CTG AAC CAG GAG CTC TGC TTG GGA CGT CCC 480  
 Tyr Arg Gly Cys Gly Ser Leu Asn Gln Glu Leu Cys Leu Gly Arg Pro  
 65 70 75 80

ACG GAG TTT CTG AAC CAT CAC TGC TGC TAT AGA TCC TTC TGC AAC CAC 528  
 Thr Glu Phe Leu Asn His His Cys Cys Tyr Arg Ser Phe Cys Asn His  
 85 90 95

AAC GTG TCT CTG ATG CTG GAG GCC ACC CAA ACT CCT TCG GAG GAG CCA 576  
 Asn Val Ser Leu Met Leu Glu Ala Thr Gln Thr Pro Ser Glu Glu Pro  
 100 105 110

GAA GTT GAT GCC CAT CTG CCT CTG ATC CTG GGT CCT GTG CTG GCC TTG 624  
 Glu Val Asp Ala His Leu Pro Leu Ile Leu Gly Pro Val Leu Ala Leu  
 115 120 125

CCG GTC CTG GTG GCC CTG GGT GGT CTG GGC TTG TGG CGT GTC CGG CGG 672  
 Pro Val Leu Val Ala Leu Gly Ala Leu Gly Leu Trp Arg Val Arg Arg  
 130 135 140

AGG CAG GAG AAG CAG CGG GAT TTG CAC AGT GAC CTG GGC GAG TCC AGT 720  
 Arg Gln Glu Lys Gln Arg Asp Leu His Ser Asp Leu Gly Glu Ser Ser  
 145 150 155 160

CTG ATC CTG AAG GCA TCT GAA CAG GCA GAC AGC ATG TTG GGG GAC TTC 768  
 Leu Ile Leu Lys Ala Ser Glu Gln Ala Asp Ser Met Leu Gly Asp Phe  
 165 170 175

CTG GAC AGC GAC TGT ACC ACG GGC AGC GGC TCG GGG CTC CCC TTC TTG 816  
 Leu Asp Ser Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe Leu  
 180 185 190

GTG CAG AGG ACG GTA GCT CGG CAG GTT GCG CTG GTA GAG TGT GTG GGA 864  
 Val Gln Arg Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val Gly  
 195 200 205

AAG GGC CGA TAT GGC GAG GTG TGG CGC GGT TCG TGG CAT GGC GAA AGC 912  
 Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Ser Trp His Gly Glu Ser  
 210 215 220

GTG GCG GTC AAG ATT TTC TCC TCA CGA GAT GAG CAG TCC TGG TTC CGG 960  
 Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe Arg  
 225 230 235 240

GAG ACG GAG ATC TAC AAC ACA GTT CTG CTT AGA CAC GAC AAC ATC CTA 1008

full  
 32  
 cont

Glu Thr Glu Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile Leu  
 245 250 255

GGC TTC ATC GCC TCC GAC ATG ACT TCG CGG AAC TCG AGC ACG CAG CTG 1056  
 Gly Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln Leu  
 260 265 270

TGG CTC ATC ACC CAC TAC CAT GAA CAC GGC TCC CTC TAT GAC TTT CTG 1104  
 Trp Leu Ile Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe Leu  
 275 280 285

CAG AGG CAG ACG CTG GAG CCC CAG TTG GCC CTG AGG CTA GCT GTG TCC 1152  
 Gln Arg Gln Thr Leu Glu Pro Gln Leu Ala Leu Arg Leu Ala Val Ser  
 290 295 300

CCG GCC TGC GGC CTG GCG CAC CTA CAT GTG GAG ATC TTT GGC ACT CAA 1200  
 Pro Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr Gln  
 305 310 315 320

GGC AAA CCA GCC ATT GCC CAT CGT GAC CTC AAG AGT CGC AAT GTG CTG 1248  
 Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Arg Asn Val Leu  
 325 330 335

GTC AAG AGT AAC TTG CAG TGT TGC ATT GCA GAC CTG GGA CTG GCT GTG 1296  
 Val Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala Val  
 340 345 350

ATG CAC TCA CAA AGC AAC GAG TAC CTG GAT ATC GGC AAC ACA CCC CGA 1344  
 Met His Ser Gln Ser Asn Glu Tyr Leu Asp Ile Gly Asn Thr Pro Arg  
 355 360 365

GTG GGT ACC AAA AGA TAC ATG GCA CCC CAG GTG CTG GAT GAG CAC ATC 1392  
 Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu His Ile  
 370 375 380

CGC ACA GAC TGC TTT GAG TCG TAC AAG TGG ACA GAC ATC TGG GCC TTT 1440  
 Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala Phe  
 385 390 395 400

GGC CTA GTG CTA TGG GAG ATC GCC CGG CGG ACC ATC ATC AAT GGC ATT 1488  
 Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Ile Asn Gly Ile  
 405 410 415

GTG GAG GAT TAC AGG CCA CCT TTC TAT GAC ATG GTA CCC AAT GAC CCC 1536  
 Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Met Val Pro Asn Asp Pro  
 420 425 430

AGT TTT GAG GAC ATG AAA AAG GTG GTG TGC GTT GAC CAG CAG ACA CCC 1584  
 Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro  
 435 440 445

ACC ATC CCT AAC CGG CTG GCT GCA GAT CCG GTC CTC TCC GGG CTG GCC 1632  
 Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala  
 450 455 460

CAG ATG ~~ATG~~ AGA GAG TGC TGG TAC CCC AAC CCC TCT GCT CGC CTC ACC 1680  
 Gln Met ~~Met~~ Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr  
 465 470 475 480  
  
 GCA CTG CGC ~~ATA~~ AAG AAG ACA TTG CAG AAG CTC AGT CAC AAT CCA GAG 1728  
 Ala Leu Arg ~~Ile~~ Lys Lys Thr Leu Gln Lys Leu Ser His Asn Pro Glu  
 485 490 495  
  
 AAG CCC AAA GTG ~~ATT~~ CAC TAGCCCAGGG CCACCAGGCT TCCTCTGCCT 1776  
 Lys Pro Lys Val ~~Ile~~ His  
 500  
  
 AAAGTGTGTG CTGGGGAAGA AGACATAGCC TGTCTGGGTA GAGGGAGTGA AGAGAGTGTG 1836  
 CACGCTGCCC TGTGTGTGCC TGCTCAGCTT GCTCCCAGCC CATCCAGCCA AAAATACAGC 1896  
 TGAGCTGAAA TTCAAAAAAA AAAAAA 1922

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Thr Leu Gly Ser Phe Arg Arg Gly Leu Leu Met Leu Ser Val Ala  
 1 5 10 15  
 Leu Gly Leu Thr Gln Gly Arg Leu Ala Lys Pro Ser Lys Leu Val Asn  
 20 25 30  
 Cys Thr Cys Glu Ser Pro His Cys Lys Arg Pro Phe Cys Gln Gly Ser  
 35 40 45  
 Trp Cys Thr Val Val Leu Val Arg Glu Gln Gly Arg His Pro Gln Val  
 50 55 60  
 Tyr Arg Gly Cys Gly Ser Leu Asn Gln Glu Leu Cys Leu Gly Arg Pro  
 65 70 75 80  
 Thr Glu Phe Leu Asn His His Cys Cys Tyr Arg Ser Phe Cys Asn His  
 85 90 95  
 Asn Val Ser Leu Met Leu Glu Ala Thr Gln Thr Pro Ser Glu Glu Pro  
 100 105 110  
 Glu Val Asp Ala His Leu Pro Leu Ile Leu Gly Pro Val Leu Ala Leu  
 115 120 125  
 Pro Val Leu Val Ala Leu Gly Ala Leu Gly Leu Trp Arg Val Arg Arg



130

135

140

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Arg<br>145 | Gln        | Glu        | Lys        | Gln        | Arg<br>150 | Asp        | Leu        | His        | Ser        | Asp<br>155 | Leu        | Gly        | Glu        | Ser        | Ser<br>160 |
| Leu        | Ile        | Leu        | Lys        | Ala<br>165 | Ser        | Glu        | Gln        | Ala        | Asp<br>170 | Ser        | Met        | Leu        | Gly        | Asp<br>175 | Phe        |
| Leu        | Asp        | Ser        | Asp<br>180 | Cys        | Thr        | Thr        | Gly        | Ser<br>185 | Gly        | Ser        | Gly        | Leu        | Pro<br>190 | Phe        | Leu        |
| Val        | Gln        | Arg<br>195 | Thr        | Val        | Ala        | Arg        | Gln<br>200 | Val        | Ala        | Leu        | Val        | Glu<br>205 | Cys        | Val        | Gly        |
| Lys        | Gly<br>210 | Arg        | Tyr        | Gly        | Glu        | Val<br>215 | Trp        | Arg        | Gly        | Ser        | Trp<br>220 | His        | Gly        | Glu        | Ser        |
| Val<br>225 | Ala        | Val        | Lys        | Ile        | Phe<br>230 | Ser        | Ser        | Arg        | Asp        | Glu<br>235 | Gln        | Ser        | Trp        | Phe        | Arg<br>240 |
| Gln        | Thr        | Glu        | Ile        | Tyr<br>245 | Asn        | Thr        | Val        | Leu        | Leu<br>250 | Arg        | His        | Asp        | Asn        | Ile<br>255 | Leu        |
| Gly        | Phe        | Ile        | Ala<br>260 | Ser        | Asp        | Met        | Thr        | Ser<br>265 | Arg        | Asn        | Ser        | Ser        | Thr<br>270 | Gln        | Leu        |
| Trp        | Leu        | Ile        | Thr        | His        | Tyr        | His        | Glu<br>280 | His        | Gly        | Ser        | Leu        | Tyr<br>285 | Asp        | Phe        | Leu        |
| Gln        | Arg<br>290 | Gln        | Thr        | Leu        | Glu        | Pro<br>295 | Gln        | Leu        | Ala        | Leu        | Arg<br>300 | Leu        | Ala        | Val        | Ser        |
| Pro<br>305 | Ala        | Cys        | Gly        | Leu        | Ala<br>310 | His        | Leu        | His        | Val        | Glu<br>315 | Ile        | Phe        | Gly        | Thr        | Gln<br>320 |
| Gly        | Lys        | Pro        | Ala<br>325 | Ile        | Ala        | His        | Arg        | Asp        | Leu<br>330 | Lys        | Ser        | Arg        | Asn        | Val<br>335 | Leu        |
| Val        | Lys        | Ser        | Asn<br>340 | Leu        | Gln        | Cys        | Cys        | Ile<br>345 | Ala        | Asp        | Leu        | Gly        | Leu<br>350 | Ala        | Val        |
| Met        | His<br>355 | Ser        | Gln        | Ser        | Asn        | Glu        | Tyr<br>360 | Leu        | Asp        | Ile        | Gly        | Asn<br>365 | Thr        | Pro        | Arg        |
| Val<br>370 | Gly        | Thr        | Lys        | Arg        | Tyr        | Met<br>375 | Ala        | Pro        | Glu        | Val        | Leu<br>380 | Asp        | Glu        | His        | Ile        |
| Arg<br>385 | Thr        | Asp        | Cys        | Phe        | Glu<br>390 | Ser        | Tyr        | Lys        | Trp        | Thr<br>395 | Asp        | Ile        | Trp        | Ala        | Phe<br>400 |
| Gly        | Leu        | Val        | Leu        | Trp<br>405 | Glu        | Ile        | Ala        | Arg        | Arg<br>410 | Thr        | Ile        | Ile        | Asn        | Gly<br>415 | Ile        |
| Val        | Glu        | Asp        | Tyr<br>420 | Arg        | Pro        | Pro        | Phe        | Tyr<br>425 | Asp        | Met        | Val        | Pro        | Asn<br>430 | Asp        | Pro        |

Sub  
32  
cont

Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro  
 435 440 445

Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala  
 450 455 460

Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr  
 465 470 475 480

Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Leu Ser His Asn Pro Glu  
 485 490 495

Lys Pro Lys Val Ile His  
 500

## (2) INFORMATION FOR SEQ ID NO: 13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2070 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 217..1812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATTCATGAGA TGGAAGCATA GGTCAAAGCT GTTCGGAGAA ATTGGAAC TA CAGTTTTATC 60

TAGCCACATC TCTGAGAATT CTGAAGAAAG CAGCAGGTGA AAGTCATTGC CAAGTGATTT 120

TGTTCTGTAA GGAAGCCTCC CTCATTCACT TACACCAGTG AGACAGCAGG ACCAGTCATT 180

CAAAGGGCCG TGTACAGGAC GCGTGGCAAT CAGACA ATG ACT CAG CTA TAC ACT 234  
 Met Thr Gln Leu Tyr Thr  
 1 5

TAC ATC AGA TTA CTG GGA GCC TGT CTG TTC ATC ATT TCT CAT GTT CAA 282  
 Tyr Ile Arg Leu Leu Gly Ala Cys Leu Phe Ile Ile Ser His Val Gln  
 10 15 20

Sub  
32  
cont

GGG CAG AAT CTA GAT AGT ATG CTC CAT GGC ACT GGT ATG AAA TCA GAC 330  
Gly Gln Asn Leu Asp Ser Met Leu His Gly Thr Gly Met Lys Ser Asp  
25 30 35

TTG GAC CAG AAG AAG CCA GAA AAT GGA GTG ACT TTA GCA CCA GAG GAT 378  
Leu Asp Gln Lys Lys Pro Glu Asn Gly Val Thr Leu Ala Pro Glu Asp  
40 45 50

ACC TTG CCT TTC TTA AAG TGC TAT TGC TCA GGA CAC TGC CCA GAT GAT 426  
Thr Leu Pro Phe Leu Lys Cys Tyr Cys Ser Gly His Cys Pro Asp Asp  
55 60 65 70

GCT ATT AAT AAC ACA TGC ATA ACT AAT GGC CAT TGC TTT GCC ATT ATA 474  
Ala Ile Asn Asn Thr Cys Ile Thr Asn Gly His Cys Phe Ala Ile Ile  
75 80 85

GAA GAA GAT GAT CAG GGA GAA ACC ACA TTA ACT TCT GGG TGT ATG AAG 522  
Glu Glu Asp Asp Gln Gly Glu Thr Thr Leu Thr Ser Gly Cys Met Lys  
90 95 100

TAT GAA GGC TCT GAT TTT CAA TGC AAG GAT TCA CCG AAA GCC CAG CTA 570  
Tyr Glu Gly Ser Asp Phe Gln Cys Lys Asp Ser Pro Lys Ala Gln Leu  
105 110 115

CGC AGG ACA ATA GAA TGT TGT CGG ACC AAT TTG TGC AAC CAG TAT TTG 618  
Arg Arg Thr Ile Glu Cys Cys Arg Thr Asn Leu Cys Asn Gln Tyr Leu  
120 125 130

CAG CCT ACA CTG CCC CCT GTT GTT ATA GGT CCG TTC TTT GAT GGC AGC 666  
Gln Pro Thr Leu Pro Pro Val Val Ile Gly Pro Phe Phe Asp Gly Ser  
135 140 145 150

ATC CGA TGG CTG GTT GTG CTC ATT TCC ATG GCT GTC TGT ATA GTT GCT 714  
Ile Arg Trp Leu Val Val Leu Ile Ser Met Ala Val Cys Ile Val Ala  
155 160 165

ATG ATC ATC TTC TCC AGC TGC TTT TGC TAT AAG CAT TAT TGT AAG AGT 762  
Met Ile Ile Phe Ser Ser Cys Phe Cys Tyr Lys His Tyr Cys Lys Ser  
170 175 180

ATC TCA AGC AGG GGT CGT TAC AAC CGT GAT TTG GAA CAG GAT GAA GCA 810  
Ile Ser Ser Arg Gly Arg Tyr Asn Arg Asp Leu Glu Gln Asp Glu Ala  
185 190 195

TTT ATT CCA GTA GGA GAA TCA TTG AAA GAC CTG ATT GAC CAG TCC CAA 858  
Phe Ile Pro Val Gly Glu Ser Leu Lys Asp Leu Ile Asp Gln Ser Gln  
200 205 210

AGC TCT GGG AGT GGA TCT GGA TTG CCT TTA TTG GTT CAG CGA ACT ATT 906  
Ser Ser Gly Ser Gly Ser Gly Leu Pro Leu Leu Val Gln Arg Thr Ile  
215 220 225 230

GCC AAA CAG ATT CAG ATG GTT CGG CAG GTT GGT AAA GGC CGC TAT GGA 954  
Ala Lys Gln Ile Gln Met Val Arg Gln Val Gly Lys Gly Arg Tyr Gly  
235 240 245

Seq  
32  
cont

GAA GTA TGG ATG GGT AAA TGG CGT GGT GAA AAA GTG GCT GTC AAA GTG 1002  
 Glu Val Trp Met Gly Lys Trp Arg Gly Glu Lys Val Ala Val Lys Val  
 250 255 260

TTT TTT ACC ACT GAA GAA GCT AGC TGG TTT AGA GAA ACA GAA ATC TAC 1050  
 Phe Phe Thr Thr Glu Glu Ala Ser Trp Phe Arg Glu Thr Glu Ile Tyr  
 265 270 275

CAG ACG GTG TTA ATG CGT CAT GAA AAT ATA CTT GGT TTT ATA GCT GCA 1098  
 Gln Thr Val Leu Met Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala  
 280 285 290

GAC ATT AAA GGC ACT GGT TCC TGG ACT CAG CTG TAT TTG ATT ACT GAT 1146  
 Asp Ile Lys Gly Thr Gly Ser Trp Thr Gln Leu Tyr Leu Ile Thr Asp  
 295 300 305 310

TAC CAT GAA AAT GGA TCT CTC TAT GAC TTC CTG AAA TGT GCC ACA CTA 1194  
 Tyr His Glu Asn Gly Ser Leu Tyr Asp Phe Leu Lys Cys Ala Thr Leu  
 315 320 325

GAC ACC AGA GCC CTA CTC AAG TTA GCT TAT TCT GCT GCT TGT GGT CTG 1242  
 Asp Thr Arg Ala Leu Leu Lys Leu Ala Tyr Ser Ala Ala Cys Gly Leu  
 330 335 340

TCC CAC CTC CAC ACA GAA ATT TAT GGT ACC CAA GGG AAG CCT GCA ATT 1290  
 Cys His Leu His Thr Glu Ile Tyr Gly Thr Gln Gly Lys Pro Ala Ile  
 345 350 355

GCT CAT CGA GAC CTG AAG AGC AAA AAC ATC CTT ATT AAG AAA AAT GGA 1338  
 Ala His Arg Asp Leu Lys Ser Lys Asn Ile Leu Ile Lys Lys Asn Gly  
 360 365 370

AGT TGC TGT ATT GCT GAC CTG GGC CTA GCT GTT AAA TTC AAC AGT GAT 1386  
 Ser Cys Cys Ile Ala Asp Leu Gly Leu Ala Val Lys Phe Asn Ser Asp  
 375 380 385 390

ACA AAT GAA GTT GAC ATA CCC TTG AAT ACC AGG GTG GGC ACC AAG CGG 1434  
 Thr Asn Glu Val Asp Ile Pro Leu Asn Thr Arg Val Gly Thr Lys Arg  
 395 400 405

TAC ATG GCT CCA GAA GTG CTG GAT GAA AGC CTG AAT AAA AAC CAT TTC 1482  
 Tyr Met Ala Pro Glu Val Leu Asp Glu Ser Leu Asn Lys Asn His Phe  
 410 415 420

CAG CCC TAC ATC ATG GCT GAC ATC TAT AGC TTT GGT TTG ATC ATT TGG 1530  
 Gln Pro Tyr Ile Met Ala Asp Ile Tyr Ser Phe Gly Leu Ile Ile Trp  
 425 430 435

GAA ATG GCT CGT CGT TGT ATT ACA GGA GGA ATC GTG GAG GAA TAT CAA 1578  
 Glu Met Ala Arg Arg Cys Ile Thr Gly Gly Ile Val Glu Glu Tyr Gln  
 440 445 450

TTA CCA TAT TAC AAC ATG GTG CCC AGT GAC CCA TCC TAT GAG GAC ATG 1626  
 Leu Pro Tyr Tyr Asn Met Val Pro Ser Asp Pro Ser Tyr Glu Asp Met  
 455 460 465 470

CGT GAG GTT GTG TGT GTG AAA CGC TTG CGG CCA ATC GTG TCT AAC CGC 1674  
 Arg Glu Val Val Cys Val Lys Arg Leu Arg Pro Ile Val Ser Asn Arg  
 475 480 485

TGG AAC AGC GAT GAA TGT CTT CGA GCA GTT TTG AAG CTA ATG TCA GAA 1722  
 Trp Asn Ser Asp Glu Cys Leu Arg Ala Val Leu Lys Leu Met Ser Glu  
 490 495 500

TGT TGG GCC CAT AAT CCA GCC TCC AGA CTC ACA GCT TTG AGA ATC AAG 1770  
 Cys Trp Ala His Asn Pro Ala Ser Arg Leu Thr Ala Leu Arg Ile Lys  
 505 510 515

AAG ACA CTT GCA AAA ATG GTT GAA TCC CAG GAT GTA AAG ATT 1812  
 Lys Thr Leu Ala Lys Met Val Glu Ser Gln Asp Val Lys Ile  
 520 525 530

TGACAATTAA ACAATTTTGA GGGAGAATTT AGACTGCAAG AACTTCTTCA CCCAAGGAAT 1872

GGGTGGGATT AGCATGGAAT AGGATGTTGA CTTGGTTTCC AGACTCCTTC CTCTACATCT 1932

TGACAGGCTG CTAACAGTAA ACCTTACCGT ACTCTACAGA ATACAAGATT GGAAGTTGGA 1992

ACTTCAAACA TGTCATTCTT TATATATGAC AGCTTTGTTT TAATGTGGGG TTTTTTTGTT 2052

TCCTTTTTTTT GTTTTGT 2070

## (2) INFORMATION FOR SEQ ID NO: 14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met Thr Gln Leu Tyr Thr Tyr Ile Arg Leu Leu Gly Ala Cys Leu Phe  
 1 5 10 15

Ile Ile Ser His Val Gln Gly Gln Asn Leu Asp Ser Met Leu His Gly  
 20 25 30

Thr Gly Met Lys Ser Asp Leu Asp Gln Lys Lys Pro Glu Asn Gly Val  
 35 40 45

Thr Leu Ala Pro Glu Asp Thr Leu Pro Phe Leu Lys Cys Tyr Cys Ser  
 50 55 60

Gly His Cys Pro Asp Asp Ala Ile Asn Asn Thr Cys Ile Thr Asn Gly  
 65 70 75 80

His Cys Phe Ala Ile Ile Glu Glu Asp Asp Gln Gly Glu Thr Thr Leu  
 85 90 95

Thr Ser Gly Cys Met Lys Tyr Glu Gly Ser Asp Phe Gln Cys Lys Asp  
 100 105 110  
 Ser Pro Lys Ala Gln Leu Arg Arg Thr Ile Glu Cys Cys Arg Thr Asn  
 115 120 125  
 Leu Cys Asn Gln Tyr Leu Gln Pro Thr Leu Pro Val Val Ile Gly  
 130 135 140  
 Pro Phe Phe Asp Gly Ser Ile Arg Trp Leu Val Val Leu Ile Ser Met  
 145 150 155 160  
 Ala Val Cys Ile Val Ala Met Ile Ile Phe Ser Ser Cys Phe Cys Tyr  
 165 170 175  
 Lys His Tyr Cys Lys Ser Ile Ser Ser Arg Gly Arg Tyr Asn Arg Asp  
 180 185 190  
 Leu Glu Gln Asp Glu Ala Phe Ile Pro Val Gly Glu Ser Leu Lys Asp  
 195 200 205  
 Leu Ile Asp Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly Leu Pro Leu  
 210 215 220  
 Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val Arg Gln Val  
 225 230 235 240  
 Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp Arg Gly Glu  
 245 250 255  
 Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala Ser Trp Phe  
 260 265 270  
 Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His Glu Asn Ile  
 275 280 285  
 Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser Trp Thr Gln  
 290 295 300  
 Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu Tyr Asp Phe  
 305 310 315 320  
 Leu Lys Cys Ala Thr Leu Asp Thr Arg Ala Leu Leu Lys Leu Ala Tyr  
 325 330 335  
 Ser Ala Ala Cys Gly Leu Cys His Leu His Thr Glu Ile Tyr Gly Thr  
 340 345 350  
 Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys Asn Ile  
 355 360 365  
 Leu Ile Lys Lys Asn Gly Ser Cys Cys Ile Ala Asp Leu Gly Leu Ala  
 370 375 380  
 Val Lys Phe Asn Ser Asp Thr Asn Glu Val Asp Ile Pro Leu Asn Thr

Sub  
 32  
 cont

**C** **2** **E** **A** **T** **H** **L**

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F2  
cont

- ```
(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 2160 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: unknown
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Mouse

(ix) FEATURE:
    (A) NAME/KEY: CDS
    (B) LOCATION: 10..1524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:
```

CGCGGTTAC ATG GCG GAG TCG GCC GGA GCC TCC TCC TTC TTC CCC CTT 48  
Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Pro Leu  
1 5 10

GTT GTC CTC CTG CTC GCC GGC AGC GGC GGG TCC GGG CCC CGG GGG ATC 96  
Val Val Leu Leu Leu Ala Gly Ser Gly Gly Ser Gly Pro Arg Gly Ile  
15 20 25

CAG GCT CTG CTG TGT GCG TGC ACC AGC TGC CTA CAG ACC AAC TAC ACC 144  
Gln Ala Leu Leu Cys Ala Cys Thr Ser Cys Leu Gln Thr Asn Tyr Thr  
30 35 40 45

TGT GAG ACA GAT GGG GCT TGC ATG GTC TCC ATC TTT AAC CTG GAT GGC 192  
Cys Glu Thr Asp Gly Ala Cys Met Val Ser Ile Phe Asn Leu Asp Gly  
50 55 60

GTG GAG CAC CAT GTA CGT ACC TGC ATC CCC AAG GTG GAG CTG GTT CCT 240  
Val Glu His His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro  
65 70 75

GGA AAG CCC TTC TAC TGC CTG AGT TCA GAG GAT CTG CGC AAC ACA 288  
Gly Lys Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr  
80 85 90

TGC TGC TAT ATT GAC TTC TGC AAC AAG ATT GAC CTC AGG GTC CCC 336  
Cys Cys Tyr Ile Asp Phe Cys Asn Lys Ile Asp Leu Arg Val Pro  
95 100 105

GGA CAC CTC AAG GAG CCT GCG CAC CCC TCC ATG TGG GGC CCT GTG 384  
Ser Gly His Leu Lys Glu Pro Ala His Pro Ser Met Trp Gly Pro Val  
110 115 120 125

CTG GTC GGC ATC ATC GCC GGC CCC CTC TTC CTC CTC TTC CTT ATC 432  
Glu Leu Val Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile  
130 135 140

ATT ATC ATC GTC TTC CTG GTC ATC AAC TAT CAC CAG CGT GTC TAC CAT 480  
Ile Ile Ile Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His  
145 150 155

AAC CGC CAG AGG TTG GAC ATG GAG GAC CCC TCT TGC GAG ATG TGT CTC 528  
Asn Arg Gln Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met Cys Leu  
160 165 170

TCC AAA GAC AAG ACG CTC CAG GAT CTC GTC TAC GAC CTC TCC ACG TCA 576  
Ser Lys Asp Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser Thr Ser  
175 180 185

GGG TCT GGC TCA GGG TTA CCC CTT TTT GTC CAG CGC ACA GTG GCC CGA 624  
Gly Ser Gly Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val Ala Arg  
190 195 200 205

ACC ATT GTT TTA CAA GAG ATT ATC GGC AAG GGC CGG TTC GGG GAA GTA 672  
Thr Ile Val Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe Gly Glu Val



210

215

220

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| TGG | CGT | GGT | CGC | TGG | AGG | GGT | GGT | GAC | GTG | GCT | GTG | AAA | ATC | TTC | TCT | 720  |
| Trp | Arg | Gly | Arg | Trp | Arg | Gly | Gly | Asp | Val | Ala | Val | Lys | Ile | Phe | Ser |      |
|     |     | 225 |     |     |     |     |     | 230 |     |     |     |     | 235 |     |     |      |
| TCT | CGT | GAA | GAA | CGG | TCT | TGG | TTC | CGT | GAA | GCA | GAG | ATC | TAC | CAG | ACC | 768  |
| Ser | Arg | Glu | Glu | Arg | Ser | Trp | Phe | Arg | Glu | Ala | Glu | Ile | Tyr | Gln | Thr |      |
|     |     | 240 |     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |      |
| GTC | ATG | CTG | CGC | CAT | GAA | AAC | ATC | CTT | GGC | TTT | ATT | GCT | GCT | GAC | AAT | 816  |
| Val | Met | Leu | Arg | His | Glu | Asn | Ile | Leu | Gly | Phe | Ile | Ala | Ala | Asp | Asn |      |
|     |     | 255 |     |     |     | 260 |     |     |     |     | 265 |     |     |     |     |      |
| AAA | GAT | AAT | GGC | ACC | TGG | ACC | CAG | CTG | TGG | CTT | GTC | TCT | GAC | TAT | CAC | 864  |
| Lys | Asp | Asn | Gly | Thr | Trp | Thr | Gln | Leu | Trp | Leu | Val | Ser | Asp | Tyr | His |      |
| 270 |     |     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |      |
| GAG | CAT | GGC | TCA | CTG | TTT | GAT | TAT | CTG | AAC | CGC | TAC | ACA | GTG | ACC | ATT | 912  |
| Glu | His | Gly | Ser | Leu | Phe | Asp | Tyr | Leu | Asn | Arg | Tyr | Thr | Val | Thr | Ile |      |
|     |     |     |     | 290 |     |     |     |     | 295 |     |     |     | 300 |     |     |      |
| GAG | GGA | ATG | ATT | AAG | CTA | GCC | TTG | TCT | GCA | GCC | AGT | GGT | TTG | GCA | CAC | 960  |
| Glu | Gly | Met | Ile | Lys | Leu | Ala | Leu | Ser | Ala | Ala | Ser | Gly | Leu | Ala | His |      |
|     |     |     | 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |      |
| CTG | CAT | ATG | GAG | ATT | GTG | GGC | ACT | CAA | GGG | AAG | CCG | GGA | ATT | GCT | CAT | 1008 |
| Leu | His | Met | Glu | Ile | Val | Gly | Thr | Gln | Gly | Lys | Pro | Gly | Ile | Ala | His |      |
|     |     | 320 |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |      |
| CGA | GAC | TTG | AAG | TCA | AAG | AAC | ATC | CTG | GTG | AAA | AAA | AAT | GGC | ATG | TGT | 1056 |
| Arg | Asp | Leu | Lys | Ser | Lys | Asn | Ile | Leu | Val | Lys | Lys | Asn | Gly | Met | Cys |      |
|     |     | 335 |     |     |     | 340 |     |     |     |     | 345 |     |     |     |     |      |
| GCC | ATT | GCA | GAC | CTG | GGC | CTG | GCT | GTC | CGT | CAT | GAT | GCG | GTC | ACT | GAC | 1104 |
| Ala | Ile | Ala | Asp | Leu | Gly | Leu | Ala | Val | Arg | His | Asp | Ala | Val | Thr | Asp |      |
|     |     | 350 |     |     | 355 |     |     |     | 360 |     |     |     |     | 365 |     |      |
| ACC | ATA | GAC | ATT | GCT | CCA | AAT | CAG | AGG | GTG | GGG | ACC | AAA | CGA | TAC | ATG | 1152 |
| Thr | Ile | Asp | Ile | Ala | Pro | Asn | Gln | Arg | Val | Gly | Thr | Lys | Arg | Tyr | Met |      |
|     |     |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |      |
| GCT | CCT | GAA | GTC | CTT | GAC | GAG | ACA | ATC | AAC | ATG | AAG | CAC | TTT | GAC | TCC | 1200 |
| Ala | Pro | Glu | Val | Leu | Asp | Glu | Thr | Ile | Asn | Met | Lys | His | Phe | Asp | Ser |      |
|     |     |     | 385 |     |     |     | 390 |     |     |     |     | 395 |     |     |     |      |
| TTC | AAA | TGT | GCC | GAC | ATC | TAT | GCC | CTC | GGG | CTT | GTC | TAC | TGG | GAG | ATT | 1248 |
| Phe | Lys | Cys | Ala | Asp | Ile | Tyr | Ala | Leu | Gly | Leu | Val | Tyr | Trp | Glu | Ile |      |
|     |     | 400 |     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |      |
| GCA | CGA | AGA | TGC | AAT | TCT | GGA | GGA | GTC | CAT | GAA | GAC | TAT | CAA | CTG | CCG | 1296 |
| Ala | Arg | Arg | Cys | Asn | Ser | Gly | Gly | Val | His | Glu | Asp | Tyr | Gln | Leu | Pro |      |
|     |     | 415 |     |     |     | 420 |     |     |     |     | 425 |     |     |     |     |      |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| TAT TAC GAC TTA GTG CCC TCC GAC CCT TCC ATT GAG GAG ATG CGA AAG    | 1344 |
| Tyr Tyr Asp Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg Lys    |      |
| 430 435 440 445                                                    |      |
| GTT GTA TGT GAC CAG AAG CTA CGG CCC AAT GTC CCC AAC TGG TGG CAG    | 1392 |
| Val Val Cys Asp Gln Lys Leu Arg Pro Asn Val Pro Asn Trp Trp Gln    |      |
| 450 455 460                                                        |      |
| AGT TAT GAG GCC TTG CGA GTG ATG GGA AAG ATG ATG CGG GAG TGC TGG    | 1440 |
| Ser Tyr Glu Ala Leu Arg Val Met Gly Lys Met Met Arg Glu Cys Trp    |      |
| 465 470 475                                                        |      |
| TAC GCC AAT GGT GCT GCC CGT CTG ACA GCT CTG CGC ATC AAG AAG ACT    | 1488 |
| Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr    |      |
| 480 485 490                                                        |      |
| CTG TCC CAG CTA AGC GTG CAG GAA GAT GTG AAG ATT TAAGCTGTTC         | 1534 |
| Leu Ser Gln Leu Ser Val Gln Glu Asp Val Lys Ile                    |      |
| 495 500 505                                                        |      |
| CTCTGCCTAC ACAAAGAACC TGGGCAGTGA GGATGACTGC AGCCACCGTG CAAGCGTCGT  | 1594 |
| GGAGGCCTAT CCTCTTGTTT CTGCCCCGGCC CTCTGGCAGA GCCCTGGCCT GCAAGAGGGA | 1654 |
| CAGAGCCTGG GAGACGCGCG CACTCCCGTT GGGTTTGAGA CAGACACTTT TTATATTTAC  | 1714 |
| CTCCTGATGG CATGGAGACC TGAGCAAATC ATGTAGTCAC TCAATGCCAC AACTCAAAC   | 1774 |
| CTTTCAGTGG GAAGTACAGA GACCCAGTGC ATTGCGTGTG CAGGAGCGTG AGGTGCTGGG  | 1834 |
| CTCGCCAGGA GCGGCCCCCA TACCTTGTGG TCCACTGGGC TGCAGGTTTT CCTCCAGGGA  | 1894 |
| CCAGTCAACT GGCATCAAGA TATTGAGAGG AACCGGAAGT TTCTCCCTCC TTCCCGTAGC  | 1954 |
| AGTCCTGAGC CACACCATCC TTCTCATGGA CATCCGGAGG ACTGCCCCCTA GAGACACAAC | 2014 |
| CTGCTGCCTG TCTGTCCAGC CAAGTGCGCA TGTGCCGAGG TGTGTCCCAC ATTGTGCCTG  | 2074 |
| GTCTGTGCCA CGCCCGTGTG TGTGTGTGTG TGTGTGAGTG AGTGTGTGTG TGTACACTTA  | 2134 |
| ACCTGCTTGA GCTTCTGTGC ATGTGT                                       | 2160 |

## (2) INFORMATION FOR SEQ ID NO: 16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu Val Val Leu  
 1 5 10 15  
 Leu Leu Ala Gly Ser Gly Gly Ser Gly Pro Arg Gly Ile Gln Ala Leu  
 20 25 30  
 Leu Cys Ala Cys Thr Ser Cys Leu Gln Thr Asn Tyr Thr Cys Glu Thr  
 35 40 45  
 Asp Gly Ala Cys Met Val Ser Ile Phe Asn Leu Asp Gly Val Glu His  
 50 55 60  
 His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro Ala Gly Lys  
 65 70 75 80  
 Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr His Cys Cys  
 85 90 95  
 Tyr Ile Asp Phe Cys Asn Lys Ile Asp Leu Arg Val Pro Ser Gly His  
 100 105 110  
 Leu Lys Glu Pro Ala His Pro Ser Met Trp Gly Pro Val Glu Leu Val  
 115 120 125  
 Glu Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile Ile Ile Ile  
 130 135 140  
 Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His Asn Arg Gln  
 145 150 155 160  
 Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met Cys Leu Ser Lys Asp  
 165 170 175  
 Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser Thr Ser Gly Ser Gly  
 180 185 190  
 Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val Ala Arg Thr Ile Val  
 195 200 205  
 Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe Gly Glu Val Trp Arg Gly  
 210 215 220  
 Arg Trp Arg Gly Gly Asp Val Ala Val Lys Ile Phe Ser Ser Arg Glu  
 225 230 235 240  
 Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr Val Met Leu  
 245 250 255  
 Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn Lys Asp Asn  
 260 265 270  
 Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His Glu His Gly  
 275 280 285

Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Ile Glu Gly Met  
 290 295 300  
 Ile Lys Leu Ala Leu Ser Ala Ala Ser Gly Leu Ala His Leu His Met  
 305 310 315 320  
 Glu Ile Val Gly Thr Gln Gly Lys Pro Gly Ile Ala His Arg Asp Leu  
 325 330 335  
 Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Met Cys Ala Ile Ala  
 340 345 350  
 Asp Leu Gly Leu Ala Val Arg His Asp Ala Val Thr Asp Thr Ile Asp  
 355 360 365  
 Ile Ala Pro Asn Gln Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu  
 370 375 380  
 Val Leu Asp Glu Thr Ile Asn Met Lys His Phe Asp Ser Phe Lys Cys  
 385 390 395 400  
 Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp Glu Ile Ala Arg Arg  
 405 410 415  
 Cys Asn Ser Gly Gly Val His Glu Asp Tyr Gln Leu Pro Tyr Tyr Asp  
 420 425 430  
 Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg Lys Val Val Cys  
 435 440 445  
 Asp Gln Lys Leu Arg Pro Asn Val Pro Asn Trp Trp Gln Ser Tyr Glu  
 450 455 460  
 Ala Leu Arg Val Met Gly Lys Met Met Arg Glu Cys Trp Tyr Ala Asn  
 465 470 475 480  
 Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln  
 485 490 495  
 Leu Ser Val Gln Glu Asp Val Lys Ile  
 500 505

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1952 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 187..1692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

AAGCGGCGGC AGAAGTTGCC GCGGTGGTGC TCGTAGTGAG GCGCGGAGG ACCCGGGACC 60  
 TGGAAGCGG CGGCGGGTTA ACTTCGGCTG AATCACAACC ATTTGGCGCT GAGCTATGAC 120  
 AAGAGAGCAA AAAAAAGTT AAAGGAGCAA CCCGGCCATA AGTGAAGAGA GAAGTTTATT 180  
 GATAAC ATG CTC TTA CGA AGC TCT GGA AAA TTA AAT GTG GGC ACC AAG 228  
 Met Leu Leu Arg Ser Ser Gly Lys Leu Asn Val Gly Thr Lys  
 1 5 10  
 AAG GAG GAT GGA GAG AGT ACA GCC CCC ACC CCT CGG CCC AAG ATC CTA 276  
 Lys Glu Asp Gly Glu Ser Thr Ala Pro Thr Pro Arg Pro Lys Ile Leu  
 15 20 25 30  
 CGT TGT AAA TGC CAC CAC CAC TGT CCG GAA GAC TCA GTC AAC AAT ATC 324  
 Arg Cys Lys Cys His His His Cys Pro Glu Asp Ser Val Asn Asn Ile  
 35 40 45  
 TGC AGC ACA GAT GGG TAC TGC TTC ACG ATG ATA GAA GAA GAT GAC TCT 372  
 Cys Ser Thr Asp Gly Tyr Cys Phe Thr Met Ile Glu Glu Asp Asp Ser  
 50 55 60  
 GGA ATG CCT GTT GTC ACC TCT GGA TGT CTA GGA CTA GAA GGG TCA GAT 420  
 Gly Met Pro Val Val Thr Ser Gly Cys Leu Gly Leu Glu Gly Ser Asp  
 65 70 75  
 TTT CAA TGT CGT GAC ACT CCC ATT CCT CAT CAA AGA AGA TCA ATT GAA 468  
 Phe Gln Cys Arg Asp Thr Pro Ile Pro His Gln Arg Arg Ser Ile Glu  
 80 85 90  
 TGC TGC ACA GAA AGG AAT GAG TGT AAT AAA GAC CTC CAC CCC ACT CTG 516  
 Cys Cys Thr Glu Arg Asn Glu Cys Asn Lys Asp Leu His Pro Thr Leu  
 95 100 105 110  
 CCT CCT CTC AAG GAC AGA GAT TTT GTT GAT GGG CCC ATA CAC CAC AAG 564  
 Pro Pro Leu Lys Asp Arg Asp Phe Val Asp Gly Pro Ile His His Lys  
 115 120 125

|                                                                 |      |
|-----------------------------------------------------------------|------|
| GCC TTG CTT ATC TCT GTG ACT GTC TGT AGT TTA CTC TTG GTC CTC ATT | 612  |
| Ala Leu Leu Ile Ser Val Thr Val Cys Ser Leu Leu Leu Val Leu Ile |      |
| 130 135 140                                                     |      |
| ATT TTA TTC TGT TAC TTC AGG TAT AAA AGA CAA GAA GCC CGA CCT CGG | 660  |
| Ile Leu Phe Cys Tyr Phe Arg Tyr Lys Arg Gln Glu Ala Arg Pro Arg |      |
| 145 150 155                                                     |      |
| TAC AGC ATT GGG CTG GAG CAG GAC GAG ACA TAC ATT CCT CCT GGA GAG | 708  |
| Tyr Ser Ile Gly Leu Glu Gln Asp Glu Thr Tyr Ile Pro Pro Gly Glu |      |
| 160 165 170                                                     |      |
| TCC CTG AGA GAC TTG ATC GAG CAG TCT CAG AGC TCG GGA AGT GGA TCA | 756  |
| Ser Leu Arg Asp Leu Ile Glu Gln Ser Gln Ser Ser Gly Ser Gly Ser |      |
| 175 180 185 190                                                 |      |
| GGC CTC CCT CTG CTG GTC CAA AGG ACA ATA GCT AAG CAA ATT CAG ATG | 804  |
| Gly Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met |      |
| 195 200 205                                                     |      |
| GGG AAG CAG ATT GGA AAA GGC CGC TAT GGC GAG GTG TGG ATG GGA AAG | 852  |
| Val Lys Gln Ile Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys |      |
| 210 215 220                                                     |      |
| TGG CGT GGA GAA AAG GTG GCT GTG AAA GTG TTC TTC ACC ACG GAG GAA | 900  |
| Tyr Arg Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu |      |
| 225 230 235                                                     |      |
| GCC AGC TGG TTC CGA GAG ACT GAG ATA TAT CAG ACG GTC CTG ATG CGG | 948  |
| Ala Ser Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg |      |
| 240 245 250                                                     |      |
| CAT GAG AAT ATT CTG GGG TTC ATT GCT GCA GAT ATC AAA GGG ACT GGG | 996  |
| His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly |      |
| 255 260 265 270                                                 |      |
| TCC TGG ACT CAG TTG TAC CTC ATC ACA GAC TAT CAT GAA AAC GGC TCC | 1044 |
| Ser Trp Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser |      |
| 275 280 285                                                     |      |
| CTT TAT GAC TAT CTG AAA TCC ACC ACC TTA GAC GCA AAG TCC ATG CTG | 1092 |
| Leu Tyr Asp Tyr Leu Lys Ser Thr Thr Leu Asp Ala Lys Ser Met Leu |      |
| 290 295 300                                                     |      |
| AAG CTA GCC TAC TCC TCT GTC AGC GGC CTA TGC CAT TTA CAC ACG GAA | 1140 |
| Lys Leu Ala Tyr Ser Ser Val Ser Gly Leu Cys His Leu His Thr Glu |      |
| 305 310 315                                                     |      |
| ATC TTT AGC ACT CAA GGC AAG CCA GCA ATC GCC CAT CGA GAC TTG AAA | 1188 |
| Ile Phe Ser Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys |      |
| 320 325 330                                                     |      |

AGT AAA AAC ATC CTG GTG AAG AAA AAT GGA ACT TGC TGC ATA GCA GAC 1236  
 Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp  
 335 340 345 350

CTG GGC TTG GCT GTC AAG TTC ATT AGT GAC ACA AAT GAG GTT GAC ATC 1284  
 Leu Gly Leu Ala Val Lys Phe Ile Ser Asp Thr Asn Glu Val Asp Ile  
 355 360 365

CCA CCC AAC ACC CGG GTT GGC ACC AAG CGC TAT ATG CCT CCA GAA GTG 1332  
 Pro Pro Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Pro Pro Glu Val  
 370 375 380

CTG GAC GAG AGC TTG AAT AGA AAC CAT TTC CAG TCC TAC ATT ATG GCT 1380  
 Leu Asp Glu Ser Leu Asn Arg Asn His Phe Gln Ser Tyr Ile Met Ala  
 385 390 395

GAC ATG TAC AGC TTT GGA CTC ATC CTC TGG GAG ATT GCA AGG AGA TGT 1428  
 Asp Met Tyr Ser Phe Gly Leu Ile Leu Trp Glu Ile Ala Arg Arg Cys  
 400 405 410

GAT TCT GGA GGT ATA GTG GAA GAA TAC CAG CTT CCC TAT CAC GAC CTG 1476  
 Val Ser Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr His Asp Leu  
 415 420 425 430

GTG CCC AGT GAC CCT TCT TAT GAG GAC ATG AGA GAA ATT GTG TGC ATG 1524  
 Val Pro Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Ile Val Cys Met  
 435 440 445

AAG AAG TTA CGG CCT TCA TTC CCC AAT CGA TGG AGC AGT GAT GAG TGT 1572  
 Lys Lys Leu Arg Pro Ser Phe Pro Asn Arg Trp Ser Ser Asp Glu Cys  
 450 455 460

CTC AGG CAG ATG GGG AAG CTT ATG ACA GAG TGC TGG GCG CAG AAT CCT 1620  
 Leu Arg Gln Met Gly Lys Leu Met Thr Glu Cys Trp Ala Gln Asn Pro  
 465 470 475

GCC TCC AGG CTG ACG GCC CTG AGA GTT AAG AAA ACC CTT GCC AAA ATG 1668  
 Ala Ser Arg Leu Thr Ala Leu Arg Val Lys Lys Thr Leu Ala Lys Met  
 480 485 490

TCA GAG TCC CAG GAC ATT AAA CTC TGACGTCAGA TACTTGTGGA CAGAGCAAGA 1722  
 Ser Glu Ser Gln Asp Ile Lys Leu  
 495 500

ATTTACAGA AGCATCGTTA GCCCAAGCCT TGAACGTTAG CCTACTGCCC AGTGAGTTCA 1782

GACTTTCCTG GAAGAGAGCA CGGTGGGCAG ACACAGAGGA ACCCAGAAAC ACGGATTCAT 1842

CATGGCTTTC TGAGGAGGAG AAAGTGTGTTG GGTAAGTGTG TCAAGATATG ATGCATGTTG 1902

CTTTCTAAGA AAGCCCTGTA TTTTGAATTA CCATTTTTTT ATAAAAAAA 1952

## (2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 502 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met Leu Leu Arg Ser Ser Gly Lys Leu Asn Val Gly Thr Lys Lys Glu  
 1 5 10 15  
 Asp Gly Glu Ser Thr Ala Pro Thr Pro Arg Pro Lys Ile Leu Arg Cys  
 20 25 30  
 Lys Cys His His His Cys Pro Glu Asp Ser Val Asn Asn Ile Cys Ser  
 35 40 45  
 Thr Asp Gly Tyr Cys Phe Thr Met Ile Glu Glu Asp Asp Ser Gly Met  
 50 55 60  
 Pro Val Val Thr Ser Gly Cys Leu Gly Leu Glu Gly Ser Asp Phe Gln  
 65 70 75 80  
 Cys Arg Asp Thr Pro Ile Pro His Gln Arg Arg Ser Ile Glu Cys Cys  
 85 90 95  
 Thr Glu Arg Asn Glu Cys Asn Lys Asp Leu His Pro Thr Leu Pro Pro  
 100 105 110  
 Leu Lys Asp Arg Asp Phe Val Asp Gly Pro Ile His His Lys Ala Leu  
 115 120 125  
 Leu Ile Ser Val Thr Val Cys Ser Leu Leu Leu Val Leu Ile Ile Leu  
 130 135 140  
 Phe Cys Tyr Phe Arg Tyr Lys Arg Gln Glu Ala Arg Pro Arg Tyr Ser  
 145 150 155 160  
 Ile Gly Leu Glu Gln Asp Glu Thr Tyr Ile Pro Pro Gly Glu Ser Leu  
 165 170 175  
 Arg Asp Leu Ile Glu Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly Leu  
 180 185 190  
 Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val Lys  
 195 200 205  
 Gln Ile Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp Arg  
 210 215 220



Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala Ser  
 225 230 235 240  
 Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His Glu  
 245 250 255  
 Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser Trp  
 260 265 270  
 Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu Tyr  
 275 280 285  
 Asp Tyr Leu Lys Ser Thr Thr Leu Asp Ala Lys Ser Met Leu Lys Leu  
 290 295 300  
 Ala Tyr Ser Ser Val Ser Gly Leu Cys His Leu His Thr Glu Ile Phe  
 305 310 315 320  
 Ser Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys  
 325 330 335  
 Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp Leu Gly  
 340 345 350  
 Leu Ala Val Lys Phe Ile Ser Asp Thr Asn Glu Val Asp Ile Pro Pro  
 355 360 365  
 Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Pro Pro Glu Val Leu Asp  
 370 375 380  
 Glu Ser Leu Asn Arg Asn His Phe Gln Ser Tyr Ile Met Ala Asp Met  
 385 390 395 400  
 Tyr Ser Phe Gly Leu Ile Leu Trp Glu Ile Ala Arg Arg Cys Val Ser  
 405 410 415  
 Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr His Asp Leu Val Pro  
 420 425 430  
 Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Ile Val Cys Met Lys Lys  
 435 440 445  
 Leu Arg Pro Ser Phe Pro Asn Arg Trp Ser Ser Asp Glu Cys Leu Arg  
 450 455 460  
 Gln Met Gly Lys Leu Met Thr Glu Cys Trp Ala Gln Asn Pro Ala Ser  
 465 470 475 480  
 Arg Leu Thr Ala Leu Arg Val Lys Lys Thr Leu Ala Lys Met Ser Glu  
 485 490 495  
 Ser Gln Asp Ile Lys Leu  
 500

## (2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GCGGATCCTG TTGTGAAGGN AATATGTG

28

## (2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GCGATCCGTC GCAGTCAAAA TTTT

24

## (2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GCGGATCCGC GATATATTAA AAGCAA

26

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CGGAATTCTG GTGCCATATA

20

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ATTCAAGGGC ACATCAACTT CATTTGTGTC ACTGTTG

37

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

GCGGATCCAC CATGGCGGAG TCGGCC

26

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

AACACCGGGC CGGCGATGAT

20

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Gly Xaa Gly Xaa Xaa Gly  
1 5

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 6 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Asp Phe Lys Ser Arg Asn  
1 5

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 6 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Asp Leu Lys Ser Lys Asn  
1 5

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 6 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Gly Thr Lys Arg Tyr Met  
1 5